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GenCore version 5.1.6
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OM protein - protein search, using sw model

July 9, 2005, 13:18:09; Search time 19 Seconds (without alignments) 2992.848 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-10-659-549-3 3043 1 MALEIHMSDPMCLIENFNEQ......GEAARSCGSQQGVWSQKVWV 591

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched: Total number of hits satisfying chosen parameters:

283416

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

.PIR\_79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	guanine nucleotide	guanine nucleotide	macrophage-activat	hypothetical prote	guanylate binding	hypothetical prote	probable guanylate	hypothetical prote	plectin - human	plectin [imported]	hypothetical prote	microtubule bindin	plectin - rat	hypothetical prote	microtubule bindin	early endosome ant	hypothetical prote		microtubule-vesicl	restin - human	spindle pole body	hypothetical prote	$\mathbf{c}$	hypothetical prote	moesin - pig	chromosomal protei	apolipoprotein A-I	transport protein	M2 protein precurs
SUMMARIES	ID	A41268	S70524	A46459	S43506	149684	T17320	A84810	H86168	G02520	A59404	T22382	T13030	A39638	T49593	H90279	A57013	T50155	T23697	A43336	822695	826710	T46337	AS5094	873852	S39804	T46486	10	6229	S23325
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	Query Match Length	592	591	589	591	623	555	217	991	4574	4684	1291			862	464	1410	762	853	1392	1427	944	992	1290	1818	577	1288	429	1790	407
de	Query	64.4	62.3	58.0	57.8	44.9	8.3	7.1	7.0	5.6	5.6	5.3	5.3	5.3	5.2	5.2	5.1	5.1	5.1	5.1	5.1	5.0	5.0	5.0	5.0	4.9	4.9	4.8	4.8	4.8
	Score	1958.5	1897	1765.5	1757.5	1365.5	251.5	216	213.5	171.5	171.5	160.5	160.5	160.5	159.5	158	156.5	155.5	154.5	154.5	154.5	153	151.5	151	151	148	148	147.5	147.5	147
	Result No.	п	7	m	4	S	9	7	80	6	10	11	12	13	14	.15	16	17	18	19	20	21	22	23	24	25	26		28	. 29

30 146 4.8 586 1 B41129 31 146 4.8 742 2 S56337 32 145.5 4.8 1925 2 T001384 34 145.5 4.8 742 2 C91265 35 145 4.8 742 2 H86105 36 144 4.7 871 2 H86105 37 144 4.7 871 2 B71605 39 143.5 4.7 1875 2 B71606 40 143.5 4.7 1875 2 B71606 41 143.5 4.7 1875 2 A47297 42 142.5 4.7 1164 2 T24806 43 142.5 4.7 1872 2 A47297 44 142.5 4.7 1872 2 A47297 45 142.5 4.7 1872 2 S05517 46 4.7 1872 2 S05517 47 142 4.7 657 2 S05517	a)	nypotherical prote hypotherical prote	hypothetical prote	probable vimentin	mannosylphosphoryl	protein T16E15.12	hypothetical prote	purine NTPase (imp	myosin-like protei	myosin heavy chain	hypothetical prote	centrosome associa	· lamin - chicken	myosin heavy chain
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$\begin{array}{c} \mathbf{d} \mathbf{d} \mathbf{d} \mathbf{d} \mathbf{d} \mathbf{d} \mathbf{d} d$	B41129	T01384	T00337	H86105	S78475	D86355	E71606	B90395	S38173	A47297	T24806	T08621	805517	A41604
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	30	32	33	35	36	37	38	33	40	41	42	43	44	45

## ALIGNMENTS

	RESULT 1 A41268		
	guanine n C:Species	icleot Homo	guanine nucleotide-binding protein 1 - human C:Species: Homo saniens (man)
	C;Date: 17-Jul-1992	7-Jul-	-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
	Richeng,	S. S.	
	A;Title:	Interf	
	A; Accession: A41268	on: A4	41268
	A; Residues: 1-592 <che></che>	3: 1-5	
	A;Cross-ret C;Genetics:	ererer 3:	A;Cross-reterences: UNIFROT:F32455; GB:M55542; NID:g183001; F1DN:AAA35871.1; F1D:g18300 C;Genetics:
	A;Gene: GDB:GBP1 A;Cross-referenc	OB:GBF	A;Gene: GDB:GBP1 A;Cross-references: GDB:378351; OMIM:600411
	A, Map pos. C, Superfa	tion:	A;Map position: 1pter-1gter C;Superfamily: guanine nucleotide-binding protein 1
•	Query Match	ıtch	64.48;
	Best Loc Matches	al Si 387;	Best Local Similarity 69.4%; Pred. No. 7.6e-101; Matches 387; Conservative 71; Mismatches 89; Indels 11; Gaps 3;
	۵	Σ-	PMCLIENFNEQLKVNQEALEILSAITQPV
	qa	-Ε	
	ò	61 K	KNIKGESVASTVOSHTKGIWIWCVPHPNWPNHTLVILDTEG GDVEKADNKNDIQIFALAL 120
	qa	61 K	
	λŏ	121	LLHNVTELTDE
	qq	121	LLSSTEVYNSIGTINQQAMDQLYYVTELTHRIRSKSSPDENENEVEDSADFVSFFPDFVW 180
	ò	179/1	TLEDECLELEDGELVTPDEYLENSLRPKGGSDQRVQNFNLPRLCIQKFFPKKKCFIFDL 238
	qa	181	TIRDPSIDLEADGGPLTPDEXLIYSLKIKKGTSQKDETFNLPRLCIRKFPFKKKCFVFDR 240
	Š	239 P	ILEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRI
	DЪ	241 P	
	Š	299 V	SNAVLALAQRENSAAVQKAIAHY
	q <sub>Q</sub>	301 V	VNAISSGDLPCMENAVLALAQIENSAAVQKAIAHYEQQMGQKVQLPTESLQELLDLHRDS 360
	ò	359 E	FKDVDQSFQKELETLLDAKQNDIC
	qa	361 E	

us-10-659-549-3.rpr

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macropusqueact.varion gener 1 protein mag-1 - mouse
NyAlternate names: guanine nucleotide-binding protein 1; interferon-gamma inducible prot
C;Species: Mus musculus (house mouse)
C;Species: Muscules: Mu
                                                                                                                                                                                                                                             480
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                                                                                                                                                                                                                                                                                                          TETEKKKKEAQVKAEAEKAEAQRIJAAIQRQNEQMMQERERIJHQEQVRQ----MEIAKQNW 536
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                                                                                                                                                                                      KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL
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                                                                EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV
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A, Molacule type: mRNA
A, Molacules: 1-589 <CHE>
A, Cross-references: GB:M55544; NID:g193439; PIDN:AAA37666.1; PID:g193440
C, Genetics:
A, Gene: MAG-1
C, Superfamily: guanine nucleotide-binding protein 1
                                                                                                                                                                                                                                                                                                                                                                                                                                    LAEQQ-----KMQEQQMQVFINCFISPLPVTWRVCSSGKEGEAARSCGSQQGVW 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             541 MARQEKTLALKLOROR -----LOKDIW
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R;Schwemmle, M.
Sylowemmle, M.
Sylowemics S70524
A,Reference number: S70523
A,Reference Homospical Homosp
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                                                                                                                             ALTETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQ----MEIAKQ 534
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                                      EVKAGIYSKPGGYRLFVQKLQDLKKKYYEFPRKGIQAEEILQTYLKSKESMTDAILQTDQ
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AVKQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQ
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QLLKEQERTLALKLQEQE 558
                                                                                                                                                                                                                                                   NWLAEQQ-----KMQEQQ 547
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C;Species: Mus muscrilus (house mouse)
C;Species: Mus muscrilus (house mouse)
C;Species: Mus muscrilus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Date: 02-Jul-1996 #sequence_revision 06-Jul-1996 #text_change 09-Jul-2004
C;Date: 02-Jul-1996 #sequence_revision 06-Jul-1996 #text_change 09-Jul-2004
A;Title: 1dentification and characterization of a new gene family induced during macroph A;Reference number: A46459; MUID:92091752; PMID:1753106
A;Reference number: A46459; MUID:92091752; PMID:1753106
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Refidues: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-633 - RESA
A;Cross-references: UNIPROT:Q61594; GB:M81128; NID:9193443; PIDN:AAA37668.1; PID:919344-C;Superfamily: guanine nucleotide-binding protein 1
                        540
                                       TEAAKEIEVERIKAETABAANRELAEKQEKPELAMQQKEESYQEHVRQL---TEKMKEEQ 539
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                        TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 44.9%; Score 1365.5; DB 2; Best Local Similarity 49.3%; Pred. No. 4.5e-68; Matches 267; Conservative 112; Mismatches 150;
                                                                                                                                                                                                             guanylate binding protein - mouse
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343506
hypothetical protein - rat
hypothetical protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: 843506
G;Accession: 843506
A;Title: Molecular cloning and characterization of an isoprenylated 67 kDa protein.
A;Reference number: 843506; MUID:94198287; PMID:8148370
A;Reference number: S43506
A;Status: preliminary
A;Molecular type: mRNA
A;Residues: 1-591 <ASU>A;Residues: 1-591 <ASU>A;Coss-references: UNIPROT:Q63663; EMBL:M80367; NID:g207604; PIDN:AAA19909:1; PID:g2076
C;Superfamily: guanine nucleotide-binding protein 1
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KRTGFSLGSTVQSHTKGIWMWCVPHPKKAGQTLVLLDTEGLEDVEKGDNQNDCWIFALAV
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                                                                       EAI EVFMKNS FKDVDQS FQKELETLLDAKQNDI CKRNLEASSDYCSALLKDI FGPLEEAV
                                                                                                                                       KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL
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                                                                                                                                                                                                                                                                             LAEQQ-----KMQEQQ 547
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Best Local Similarity 63.39
Matches 346; Conservative
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Conservative
                                                              Query Match
Best Local Similarity
Matches 47; Conserv
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         A; Map position:
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probable guanylate binding protein [imported] - Arabidopsis thaliana
probable guanylate binding protein [imported] - Arabidopsis thaliana
probable guanylate binding mouse-ear cress)
C;Species: Arabidopsis thaliana [mouse-ear cress)
C;Date: 02-Peb-2001 #sequence_revision 02-Peb-2001 #text_change 09-Jul-2004
C;Accession: A84810
C;Accession: A84810
M; Koo, H; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
Nature A02, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUD:20083487; PMID:10617197
A;Accession: A84810

T17320
hypotherical protein DKFZp564J0863.1 - human (fragment)
C;Speciae; Homo sapiens (man)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
R;Dubsterbnoeft, A.; Lauber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, September 1999
A;Reference number: Z18727
A;Reference number: Z18727
A;Reference number: Z18727
A;Molecule type: mRNA
A;Residues: 1-555 cDUE>
A;Cross-references: UNIPROT:Q9UFL1; EMBL:AL117600
A;Experimental source: fetal brain; clone DKFZp564J0863
C;Genetics:
A;Note: DKFZp564J0863.1
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90 ILDFMLRYLYSQKESGHSNWLGDPEEPLTGFSWRGGSDPETTGIQIWSEVFTVEKPGGKK 149
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8.3%; Score 251.5; DB 2;
Best Local Similarity 24.9%; Pred. No. 1.2e-06;
Matches 112; Conservative 68; Mismatches 182;
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hypothetical protein [imported] - Arabidopsis thaliana C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C; Dacession: H86168
R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C., A; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A; Reference and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719; PMID:11130712
A; Accession: H86168
A; Accession: Preliminary
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                                                                                                                                                                                                                                                20 QLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAGKN--KGFSVASTVQSHTKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78 IWIWCVP---HPNWPNHTLVILDTEGLGDVEKADNKNDIQIFALALLLSSTFVYN 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ||:|| : :::||||| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| |
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9
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Length 217;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVNAISSGD-
7.1%; Score 216; DB 2;
40.9%; Pred. No. 3.5e-05;
tive 26; Mismatches 36;
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395		Db 2556 QLREEQQRQQQME 2569
Oy 398 L Db 449 -	LEASSDYCSALLKDIFGPLEEAVKQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEE 457	RESULT 10 A59404 plectin [imported] - human
Oy 458 V	VLOKYLKSKESVSHAILQTDQALTETEKKKKRAQVKAEAEKAEAQRLAAIQRQN 511	C:Species: Homo sapiens (man) C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004 C:Accession: C59404; A59404 R:Liu, C.G.; Maercker, C.; Castanon, M.J.; Hauptmann, R.; Wiche, G.
Oy 512 B		Proc. Natl. Acad. Sci. U.S.A. 93, 4278-4283, 1996 A,Title: Human plectin: organization of the gene, sequence analysis, and chromosome loc A,Reference number: C59404; MUID:96210632; PMID:8633055
558 558 607		A;Status: preliminary A;Status: preliminary A;Molecule type: DNA A;Residues: 1-4684 <sto> A;Cross-references: UNISOT:015149; GB:CAA91196; NID:g1296662; PIDN:CAA91196.1</sto>
RESULT 9 G02520 plectin - human		2
C;Species: Homo sapiens (man) C;Date: 21-Dec-1996 #sequence C;Accession: G02520 R;McLean, W.H.I.; Smith, F.J.I.	o sapiens (man) 1996 #sequence_revision 06-Jun-1997 #text_change 20-Aug-1999 12520 ::; Smith, F.J.D.	Qy 190 DGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPAHQKKLAQLE 249  b 2301 DAEMEKHKKPAEQTLRQKAQVEQELTTLRLQLESTDHQKNLL 2342
A; Reference num A; Reference num A; Accession: G0 A; Status: preli	ne Embi Data Library, march 1990 12520 minary, translated from GB/EMBL/DDBJ	QY 250 TLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVNAIS 303
A;Molecule type A;Residues: 1-4 A;Cross-referen C;Genetics:	A; Molecule type: mRNA A; Residues: 1-4574 <mcl> A; Cross-references: EMBL: U53204; NID: g1477645; PIDN: AAB05427.1; PID: g1477646 C; Genetics:</mcl>	Qy 304 SGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSE 359
A;Gene: PLEC1 C;Superfamily: 1 F;68-283/Domain	;Gene: PLEC1 ;Superfamily: plectin; alpha-actinin actin-binding domain homology; ribosomal protein \$ ;68-283/Domain: alpha-actinin actin-binding domain homology <act></act>	QY 360REALEVPMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLE 417
Query Match Best Local Sim Matches 81;	Similarity 18.7%; Pred. No. 0.46; Similarity 18.7%; Pred. No. 0.46; Indels 129; Gaps 12;	418 BAVKQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAESULQKYLKSK
Qy 190 by   190 by   190 by   191 by	190 DGQLVTPDEYLENSLRPKÇGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPAHQKKLAQLE 249	467 ESVSHAILQTD
Qy 250 TI Db 2233	TLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVNAIS 303	2548 BEIGERMAKIELAIQENVILVQIDEIQKQQSDHUAEKUKEALAELEKEKEKEKLQQEAKLLQ 499 AEAQRLAAIQRQNEQMMQERERLHQ
Qy 304 SC Db 2277 -	SGDLPCIENAVLALAGRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSE359	. 2608 LKSEEMQTVQQEC 536 WLAEQQKMQEQQMQ    : :  :
Qy 360	REALEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLE 417	Db 2666 QLREEQQRQQQME 2679 . RESULT 11
Qy 418 EJ       Db 2378 EG	EAVKQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSK 466   :	T22382 hypothetical protein F48F5.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
Qy 467 E6       Db 2438 E1	ESVSHAILQTDQALTETEKKKKEAQVKAEAEK 498   : :  :   :   :   :   :   :   :   EBIGEKLHRTELATQEKVTLVQTLEIQRQQSDHDAERLREAIAELEREKEKLQQEAKLLQ 2497	C;Accession: T22382 R;Lloyd, C. submitted to the EMBL Data Library, November 1996 A;Reference number: Z19558
Oy 499 AJ	AEAQRIAAIQRQNEQMMQERERIHQEQVRQMEIAKQN 535 ::: :   ::  :    :    :    1   1   1   1	A;Accession: T22382 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residnes: 1-1291 cWT;
536	) 	Ajcross-references: UNIPROT:09XV10; EMBL:Z81541; PIDN:CAB04411.1; GSPDB:GN00023; CESP:F4 A;Experimental source: clone F48F5 C;Genetics:

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A39638
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T13030
microtubule binding protein D-CLIP-190 - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
C;Accession: T13030
B;Lantz, V.A.; Miller, K.G.
J. Cell Biol. 140, 897-910, 1998
A;Title: A class VI unconventional myosin is associated with a homologue of a microtubul A;Accession: T13030
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              480
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                                                                                                                                                                                                                                                             NDIQIFALAL-----LLSSTFVYNTVNKIDQGA--IDLLHNVTELTDLLKARNSPDL 160
                                                                                                                                                                                                                                                                                                                           DRVEDPADSASFFPDLVWTLRDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLP 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TLPGGIMVNGSRLKNLVLTYVNAISSGDLPCIENAVLALAQRENSAAVQKAIAH----- 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      523 KIPDAMKKU-------VRAVTLELNKRSESLNQSDAISHSASALR 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----YDQQMGQ-----KVQLPME--TLQELLDLHRTS--EREAIEVFMK 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          621 AFVAKIDVSKLKTLNNYSAILKTLĖTMPDVKMBALEKSEVLBILIRAISATRRRRRAAG 680
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TETEK-----KKKEAQVKAEAEKAEAQRLAAIQRQNEQMMOERERLHQEQVRQM 529
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                                                                                                                                                                                                                          POTDDERRPGHEFMAKVKS------382
                                                                                                                                                                                                                                                                                                                                                         ESTLLPNLNNSFIQDVMFK------471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               681 SNAHLVAAKVILDKİAALDLQFSSNIAHFKNAPLAFQSFSKFLAKFF----ATQÖKİSA 735
                                                                                                                                                                                                                                                                                                                                                                                                         --CLQK-LKAKSLLVTQAIATIQKLRKL----DDKL-LESVQQTAKSVSQ-FSETLASVK
                                                                                                                                -----VNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG
                                                                                                                                                                                                                                                                                        - DVADFVKSLTFTDINNQTLSEGEIVKVVEDIKKSGKLAKIQENVKSIEDKINGIKLKNL
                                                                                                                                                                                                                                                                                                                                                                                         RLCIOKFFPKKKCFIFDLPAHOKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSM--TK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              736 SONGGGGGGGGGGGESEFPTVIVVVSIVGALLLALAAFLAFLVYGFHORKKOAKIDRDNKEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QKTEELKAKYYREPRKGIQAEE-VLQKYLKSKESVSHAI------LQTDQAL
                                                                                                  Gaps
                                                                 Query Match 5.3%; Score 160.5; DB 2; Length 1291; Best Local Similarity 18.7%; Pred. No. 0.38; Matches 143; Conservative 100; Mismatches 224; Indels 299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | :: :||::| :| : | EKSEARKIAEKKKEEDEAQKVKNIWKHIKKMRFTTLRACADFIEG 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EIAKONWLAEQOKMQEQOMOVFINCF -- ISPLP-VTWRVCSSGKEG 572
A;Gene: CESP:F48F5.1
A;Map position: 5
A;Introns: 753/2; 814/3; 987/2; 1030/3; 1114/2; 1153/3; 1222/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     369 NSFKDVDQS------FQKELETLLDAKQ-----
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                                                                                                                                14 IENFNEOLK----
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plectin - rat
Cispecies Rattus norvegicus (Norway rat)
Cispecies Rattus norvegicus (Norway rat)
Cispecies 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
Cispecies Cispecker, B:, buber, K:, Weitzer, G.; Castanon, M.J.; Hauptmann, R.; Stratowa G.; Becker, B:, buber, K.; Weitzer, G.; Call Biol. 114, 83-99, 1991
A;Title: Cloning and sequencing of rat plectin indicates a 466-kD polypeptide chain with A;Reference number: A39638, MUID:91268156; PMID:2050743
A;Status: preliminary
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A;Residues: 1-687 <WIC.>
A;Residues: 1-687 <WIC.>
A;Cross-references: UNIPROT:P30427; EMBL:X59601; NID:g1292885; PIDN:CAA42169.1; PID:g156
C;Superfamily: plectin; alpha-actinin actin-binding domain homology; ribosomal protein S
C;Keywords: cytoskeleton; transmembrane protein
F;6-103/Domain: ribosomal protein S10 homology <R810>
F;184-399/Domain: alpha-actinin actin-binding domain homology <ACT>
A, Residues: 1-1690 <LAN>
A, Residues: 1-1690 <LAN>
A; Cross-references: EMBL:AF041382; NID:92773362; PID:92773363; PIDN:AAB96783.1
A; Experimental source: strain Oregon R
C; Genetics:
A; Cross-references: FlyBase:FBgn0020503
C; Keywords: cytoskeleton
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTS---ERBAI-----EVFMKN- 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    629
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               468 TPSLOSILPP-----DLPSDDGALOBEIAOLOBKWTIQOKEVESRIAEOLEBEORLREN 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVNAISSGDLPC-IEN--AVLALAQRENSA 324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     465 SKESVSHAILQTDQALTETEKKKKEAQVKAEAEKAE------AQRLAAIQRQNEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       788 KTLGHEKL---QAALEELKKEKETIIKEKEQELQQLQSKSAESESALKVVQVQLEQLQQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DRVEDPADSASFFPDLVWTLRDFCLGLEIDGQLVTPDFYLENSLRPKQGSDQRVQNFNLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  221 RLCIQKFFPKKKCFIFDLP----AHQKKLAQLE---TLPDDELEPEFVQQ-----VTEF
                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    5.3%; Score 160.5; DB 2;
20.8%; Pred. No. 0.54;
iive 90; Mismatches 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            430 GHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 20.8%
Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                565 VCSSGKEG 572
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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545 515

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microtubule binding protein, probable [imported] - Sulfolobus solfataricus C;Species: Sulfolobus solfataricus C;Species: Sulfolobus solfataricus C;Species: Sulfolobus solfataricus C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004 C;Accession: H90279 R;Sh: O: Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; ChanJong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. A;Abescription: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:Q9UXN4; GB:AE006641; NID:g13814451; PIDN:AAK41495.1; GSPDB:G
                                                                                                                                                                   230 KKKCFIFDLPAHQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGS 289
                                                                                                                                                                                                                                                                                          290 RLKNLVLTYVNAISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQ 349
                                                                                                                                                                                                                                                                                                                                                   -----SDATDDQELTGGVFLP---- 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     287 ---EYHRRIPADGLSIYAEGIWDQIVSNKDLDLPTQQE---LLAQFRCDEIAREVQIAFD 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       404 YCSALLKDIFGPLEEAVKQGIYSKPG-----GHNLFIQKTEELKAKYYR--EPRKGIQAE 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   341 AAIAPLEEQQAESTRAGKPAVLPNLGQIGAEAREKCVKNFETQASRYHKGVYTTKRAELE 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---KESVSHAILQTDQA-----LTETEKKKKEAQ 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 401 DKIDNRLKALYQAHLTAAHKAGVTAFSEAVANAVKAGQKAGGAYEFAEIVEKQKTKTLEI 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RRAEERIAKLENAVEQLVEAQKRTDERITKL----EESTKKLE---QAVQELJEAQKKH 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EREALEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEE 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            419 AVKQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQ 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -- RPKQGSDQRVQNFNLPRLCIQKFFP 229
                                                                               194 DH-IG------VTPLANLRNTLIQDLTHIWSSISKPAGLENSKIEDY------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     461 FKKEAQSLAIPGVAMSNFKPQYLIFEKELDEVSARLRKEEMRRLAIRVERWVKSR----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 492 VKABAEKAEAQRLAAIQRQNEQMMQERE-----RLHQEQVRQMEIAKQNWLAEQQKMQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                103 SSGD--LPCIENAV--LALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LPDDEL-----EPEFVQQVTEFCSY1FSH---SMTKTLPGGIMVNGSRLKNLVLTYVNAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----LGDAIGLEFNKLGSGRGGSGAPESGEKPATEKDIW-DRVW 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            546 QQMQVFINCFISPLPVTMRVCSSGKEGEAARSCG----SQQGVWSQKVW
                                                                                                                                                                                                                           ----PDFAFAALPHKILQ----PD----KFISEVQNL-----
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                                    DFCLGLEIDGQLVTPDEYLENSL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      457 EVLOKYLKS-----
                                                                                                                                                                                                                                                                                                                                                         267 RNKD----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Accession: H90279
A;Status: preliminary
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                                    182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein B3E4.60 [imported] - Neurospora crassa
C;Species: Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C;Accession: T4953
R;Schulte, U; Aign, V; Hoheisel, J; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, May 2000
                                                                                                                                                                                                2345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2489
                                                                                                                                                                                                                                                                                                 2490 --KEQWAQQLVEBTQGFQRTLEAERQRQLEMSAEAERLKTRWAEMSRAQARAEBDAQRFR 2547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2608 LLOLKSEEMQTVQQ--EQILQETQALQKSFLSEKDSLLQRERFIEQEKAKLEQLFQDEVA 2665
                                                                         13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27;
                                                                                                                                                                                                                                                         250 TLPDDELE-----PEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVNAIS 303
                                                                                                                                                                                                                                                                                                                                                                                       304 SGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSE---- 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --REAIEVFWKNSFKDVDQSFQKELETLLDAKQNDICK---RNLEASSDYCSALLKDIFG 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLEEAVKQGIYSKPGGHNLFIQ------KTEELKAKYYREPRKGIQAEEVLQKYL 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KSKESVSHAILQTD------QALTETEKKKKEAQVKAE 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------ EQVROMEIA 532
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         126 FVYNTVNK---IDQGA-IDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTLR 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        145 LIVNIWEHQVGLYQGANMGLLKTVFEVNMQLFLKDKQNQTR-----SLLFF----VIR 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |- || : | |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |-
                                                                                                                                                                                          2304 DAEMEKHKKFAEQTLROKAQVEGELTTLRLQ------LBETDHQKSIL---
                                                                                                                              190 DGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPAHQKKLAQLE
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                                                                         Gaps
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A;Introns: 181/2; 764/1
C;Superfamily: Saccharomyces cerevisiae probable membrane protein YOR165w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 18.3%; Score 160.5; DB 1; Length 4687; Similarity 18.3%; Pred. No. 1.9; Onservative 79; Mismatches 143; Indels 135;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-862 <SCH>
A;Cross-references: UNIPROT:Q9P5X6; EMBL:AL355931; G
A;Experimental source: BAC clone B3E4; strain OR74A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              496 AEKAEAQRLAAIQRQNEQMMQERERLHQ---
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A; Status: preliminary
A; Molecule type: DNA
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Query Match
Best Local S
Matches 80
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qa	217 ELIEAĢKKHDERITKLEESTKKLEQAVĢELIEAĢKKHDERITKLE-ESIQKLVDAQRRAE 275
δγ	MOVFINCFISPL-PVTMRVCSSG
qq	276 ERIAKLENAVEQ-LVEAQKRTDERITKLEEVTWKLVESQLGMQNEIRELRKA 326
ò	578 CGSQQGVWSQ 587
qa	327 LGSWGKRWGR 336
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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No.
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Sequence 5067, App Sequence 209, Appl Sequence 29, Appl Sequence 29, Appl Sequence 10580, A Sequence 1014, App Sequence 7111, App Sequence 7112, App Sequence 7113, App Sequence 7, Appl Sequence 27, Appl Sequence 27, Appl Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 7, 6, Appli	EIN disk	4; Length 591; 254; 0; Indels 0; Gaps 0; PVVVVAIVGLYRTGKSYLMNKLAG 60 
288 4 US-09-107-532A-5067 288 4 US-09-919-039-209 531 4 US-09-418-710-29 568 4 US-09-839-479-29 568 4 US-09-839-479-29 568 4 US-09-839-016-10580 857 4 US-09-58-016-7111 984 4 US-09-949-016-7111 984 4 US-09-949-016-7113 972 4 US-09-949-016-7113 987 1 US-08-418-710-27 897 1 US-08-418-719-27 897 1 US-08-418-719-27 897 1 US-08-418-719-27 897 1 US-08-418-719-27 897 1 US-08-418-719-718-719-719-719-719-719-719-719-719-719-719	ALIGNMENTS  3 3 42024  FORMATION: CANT: Diane Pennica CANT: Diane Pennica CANT: Diane Pennica CANT: Diane Pennica CANT: Diane Pennica COF INVENTION: GUANYLATE-BINDING PROTEIN R OF SEQUENCES: 43 SPONDENCE ADDRESS: STATE: California STATE: California COUNTRY: USA ZIP: 94080 ZIP: 94080 ZIP: 94080 ZIP: 94080 ZIP: PALIGATION OF COMPATIBLE COMPUTER: IBM PC COMPATIBLE COMPATICATION DATA: MEDLICATION DATA: MEDLICATION NUMBER: US/09/643,657 FILING DATE: 19-Aug-2000 CLASSIFICATION NUMBER: 28,616 FILING DATE: 29-Jan-1998 NAWE: Hasak, Janet E. REGISTRATION NUMBER: 28,616 FILING DATE: 29-Jan-1998 NAWE: Hasak, Janet E. REGISTRATION NUMBER: 28,616 FILING DATE: 29-Jan-1998 NAWE: Hasak, Janet E. REGISTRATION NUMBER: 28,616 FILING DATE: 29-Jan-1998 NAWE: RESO/0225-1891 NEDRE SEQ ID NO: 3: NEELEPHONE: 650/225-1891 NEDRE SEQ ID NO: 3: NEED ENCRIPTION: SEQ ID NO: 3: TELENGY: SIT MIGHAET TELENGY: Linear NUCE DESCRIPTION: SEQ ID NO: 3: NUCE DESCRIPTION: SEQ ID NO: 3: NUCE DESCRIPTION: SEQ ID NO: 3: NUCE DESCRIPTION: SEQ ID NO: 3: NUCE DESCRIPTION: SEQ ID NO: 3: NUCE DESCRIPTION: SEQ ID NO: 3: NUCE DESCRIPTION: SEQ ID NO: 3:	0%; Score 3043; DB 0%; Pred. No. 1.7e- 0; Mismatches FNEQLKVNQEALEILSAITQ 
11	1 143-657-3 143-657-3 14 No. 664204 14 No. 664204 14 NO. 664204 14 NO. 664204 17 NEWEL INFORMATION: 17 NEWEL 17 NEWEL 17 NEWEL 17 NEWEL 17 SOUL  Query Match Best Local Similarity 100 Matches 591; Conservative  1 MALEIHMSDPMCLIE	
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                 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
                                                                            HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300
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                                                                                                                                                                                    HOKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300
                                                                                                                                                                                                                                                                  EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV
                                                              LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL
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APPLICANT: Bandman, Olga
APPLICANT: Au-Young, Janice
APPLICANT: Au-Young, Janice
APPLICANT: Hillman, Jennifer L.
APPLICANT: Hillman, Jennifer L.
APPLICANT: HILL OF INVESTION: NOVEL HUMAN GUANYLATE BINDING PROTEINS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyce Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
STREET: GA
COUNTRY: US
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ZIP: 343.04
ZIP: 943.04
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: EBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/736,770
FILING DATE: Filed Herewith
PRICR APPLICATION NUMBER:
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
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Patent No. 5871965
GENERAL INFORMATION:
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REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
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Sequence 8823, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OP DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-09
PRIOR FILING DATE: 2000-09-08
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                                                                                                                                                                                                                                            633;
                                                                                                                                                                                                                                         85.8%; Score 2610.5; DB 2; Length 94.4%; Pred. No. 4.8e-217; tive 8; Mismatches 20; Indels
LENGTH: 633 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                           Matches 519; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                         AAU12172-AAU12446 represent novel human secretory and transmembrane PRO
polypeptides. The PRO polypeptides are useful to detect other PRO
CC polypeptides, to link bioactive molecules to cells expressing PRO
polypeptides, to link bioactive molecules to cells expressing PRO
polypeptides, and to detect the presence of mammalian lung, colon,
CC polypeptides, and to detect the presence of mammalian lung, colon,
CC preast, prostate, rectal, cervical or liver tunours by comparing PRO
CC polypeptide expression in a cell sample to that in a control sample. Some
CC of the 275 sequences are also useful to stimulate the release of tumour
CC of the 275 sequences are also useful to stimulate the release of tumour
CC differentiation of chondrocytes, the proliferation or gene expression in
CC differentiation of inner ear utricular supporting cells or of T-
C lymphocytes, the release of procedycan from cartilage, the
CC proliferation of a cytokine from peripheral blood monocytes
(PBMCs), or the proliferation of a cytokine from peripheral blood monocytes
(PBMCs), or the proliferation of endothelial cells. Some of the PRO
CC polypeptides may modulate glucose or free fatty acid uptake by skeletal
CM muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
CM involved in binding interactions. The polymclecticides encoding PRO
CM involved in binding interactions. The polymclectices publical
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                                                                                                  Deforge L, Desnoyers L, Filvaroff E, G.
A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polypeptides can be used to generate probes, antisense RNA/DNÄ, transgenic or knock out animals and can be used in gene therapy
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                                                                                                                                                                                                                                                                                                Claim 12; Fig 46; 813pp; English
24-AUG-2000; 2000WO-US023328.
08-NOV-2000; 2000WO-US030952.
10-NOV-2000; 2000WO-US030873.
                                                                                                                                                                                                                                                                   breast, prostate, cervical.
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Matches 549; Conservative
                                                                                                 Beresini M,
E, Goddard
                                                                                                                               Stewart TA,
                                                                  (GETH ) GENENTECH INC
                                                                                                                                                                2001-408281/43.
                                                                                                                                                                             N-PSDB; AAS21266.
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                                                                                                                ME,
                                                                                                                   Gerritsen
                                                                                                  Baker KP,
                                                                                                                                 Smith V,
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The invention relates to a diagnostic composition containing at least one of 23 mucleotide sequences (I, ABLS8901-ABLS8950) with altered expression associated with tumours. (I), including antisense sequences and ribozymes, also proteins (II, ABB77424-ABB7745) encoded by them and antibodies specific for (II), are useful for diagnosis, monitoring and treatment of tumours, especially cuteneous T cell lymphoma (TCTL). (II) and antibodies to (II) are useful for vaccination. (II) can also be used to prepare pre-loaded antigen-presenting cells or tumour-specific T cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Composition containing tumor-associated nucleic acid, useful for diagnosis and treatment of tumors, especially cutaneous T cell lymphoma, also derived proteins and antibodies.
                                                                                                                                                                                      TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMQERERLHQEQVRQMEIAKQNWLAEQ
                                                                                                                                                      TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ
                                                                                KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL
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EAIBVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KNKGFSVASTVOSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL
                                                     KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL
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Pred. No. 1.2e-222;
); Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human tumour marker protein GBP-TA.
                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB77445 standard; protein; 586 AA.
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100.0%; Pre
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Best Local Similarity 100.0
Matches 549; Conservative
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2000WO-US007377.
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99WO-US000106.
99WO-US005028.
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99WO-US010733.
99WO-US012252.
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06-JAN-2000;
11-FEB-2000;
18-FEB-2000;
18-FEB-2000;
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30-MAR-2000;
17-MAY-2000;
22-MAY-2000;
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02-JUN-2000;
28-JUL-2000;
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23-AUG-2000;
24-AUG-2000;
08-NOV-2000;
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15-MAR-2000;
20-MAR-2000;
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25-MAY-2001;
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05-JAN-1999;
08-MAR-1999;
10-MAR-1999;
          29-OCT-1998;
29-OCT-1998;
20-NOV-1998;
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-DEC-1999;
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22-DEC-1999;
30-DEC-1999;
30-DEC-1999;
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28-FEB-2001;
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15-SEP-1999;
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02-JUN-1999
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29-NOV-1999
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KQGIYSKPGGHNLPIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480
                        RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240
                                                                                                          HOKKLAQLETLPDDELBPEFVQQVTEFCSYIFSHSWFKTLPGGIMVNGSRLKNLVLTYVN 300
                                                                                                                           HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300
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           LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; secreted and transmembrane protein; PRO; antiinflammatory; antiarteriosclerotic; ardiant; anti-infertility; anti-HIV; cytostatic; antidiabetic; gene therapy; tumour necrosis factor (TMF)-alpha release; TMF-alpha release; cell proliferation; cell differentiation; gene expression modulator proteoglycan release; cytokine release; tumour; inflammatory disease; organ failure; atherosclerosis; acadiac injury; infertility, birth defect; premature aping; AIDS; acquired immunodeficiency syndrome; cancer; diabetic complication; chromosome mapping; gene mapping; pharmaceutical; diagnostic; biosensor; bioreactor; tissue typing.
                                                                         RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA
                                                                                                                                                           AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGGKVQLPMETLQELLDLHRTSER
                                                                                                                                                                                                           EAIEVPMKONSPKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFQPLEEAV
                                                                                                                                                                                                                         Novel human secreted and transmembrane protein PRO4987.
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98WO-US012455.-
98WO-US017852.-
98WO-US018024.-
98WO-US019093.-
98WO-US019094.-
98WO-US019177.-
98WO-US019330.-
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31-MAR-1997; 12-JUN-1996; 14-JUN-1998; 28-AUG-1998; 10-SEP-1998; 14-SEP-1998; 14-SEP-1998; 14-SEP-1998; 16-SEP-1998; 17-SEP-1998; 17-SEP-1998;

Homo sapiens

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AISSGDLPCIENAVLALAQRENSAAVQXAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360
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                                                                                                           241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN
                                                                                                                                                                                                                                                            BAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV
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                                  181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA
                                                                                                                                                                                                                                    EAI EVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV
                                                                             HOKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN
                                                                                                                                                      AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER
                                                                                                                                                                                                                                                                                                               KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL
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97US-0056974P.
97US-0059113P.
97US-0059117P.
97US-0059122P.
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97US-0059352P.
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97US-0062285P.
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97US-0062816P.
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17-SEP-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention describes an isolated nucleic acid (I) comprising, or which has 80 % sequence identity to, or the full-length coding sequence of, one of 275 nucleotide sequences, and which encodes a corresponding col of 275 nucleotide sequences, and which encodes a corresponding col or 275 nucleotide sequences, where all sequences are given in the specification. The polypeptide encoded by (I) is used to detect PRO polypeptide, modulate a biological activity of a cell expressing a CRO polypeptide, modulate a biological activity of a cell stimulate the release of tumour necrosis factor (TNF)-alpha from human blood, modulate the proliferation or differentiation of cells, stimulate the release of cytokine crom peripheral blood emonouclear cells, inhibit the binding of A-peptide to factor VIIA, or detect the presence of tumour in a mammal. The nucleic acid and polypeptide encoded by it, are useful for treating inflammatory confiscases, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, acquired immunodeficiency syndrome confiscations. The nucleic acid is useful as hybridisation probes, in chromosome and gene mapping, and in generating antisense RNA or DNA. The polypeptides are useful in tissue typing. This is the anno acid sequence of a novel human secreted and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New secreted and transmembrane PRO nucleic acids, for treating inflammation, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, axquired immunodeficiency
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E, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
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          2001MO-US017800
2001US-00874503
2001US-00882636
2001US-00886342
2001WS-00887879
2001US-00887879
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2001WO-US021735.
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19-DEC-2001; 2001US-00028072.
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Best Local Similarity 100.
Matches 549; Conservative
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Gerritsen ME, Goddard A
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N-PSDB; ACD23875.
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09-AUG-2001;
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8 요 ò 셤 ò

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03-NOV-1997
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New isolated PRO polypeptide useful for treating diabetes, rheumatoid arthritis, sports injuries, obesity, hearing loss in mammals, stroke, heart attack.
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       06-JAN-2000; 2000WO-US000376.
11-FEB-2000; 2000WO-US001565.
18-FEB-2000; 2000WO-US004341.
18-FEB-2000; 2000WO-US004342.
22-FEB-2000; 2000WO-US004414.
24-FEB-2000; 2000WO-US006914.
24-FEB-2000; 2000WO-US006904.
                                                                                01-MAR-2000; 2000WO-US005601
02-MAR-2000; 2000WO-US005746
2000WO-US000277
                                                                                                                                Baker KP, Beresini M,
Gerritsen ME, Goddard
Smith V, Stewart TA,
                                                                                                              (GETH ) GENENTECH INC
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The present invention relates to the isolation of novel human PRO polypeptides, and the polymucleotide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides and polymuclocides are useful for preparing a medicament useful in the treatment of diabetes, bone and/or cartilage disorders (e.g. rheumatoid arthritis, sports injuries, osteoarthritis), obesity, hyper- or hypo-insulinaemia, hearing loss, and coagulation disorders (e.g. stroke, heart attack). Anti-PRO antibodies are useful in diagnostic assays for PRO, by detecting its expression in specific cells, tissues or serum, and for affinity purification of PRO from recombinant cell culture or natural sources. ABUS0870-ABUS1144 represent the human PRO polypeptides of the invention. Note: The sequence data for this patent was obtained in electronic format directly from the USPTO web site at sequata.uspto.gov/psipsDEDEntry.html 180 180 240 240 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300 9 9 61 XNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTBGLGDVEKADNKNDIQIFALAL AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFKKKKCFIFDLPA ; 0 Query Match 92.5%; Score 2815; DB 6; Length 586; Best Local Similarity 100.0%; Pred. No. 1.2e-222; Matches 549; Conservative 0; Mismatches 0; Indels Sequence 586 AA; 241 61 181 181 241 301 301 Query Match a 셤 g à 요 셤 ò g ò ઠ ð ò

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EALEVFMKONSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV

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Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Ga
Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
                                                                       2000WO-US004341.
2000WO-US004342.
2000WO-US004414.
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99WO-US031274
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N-PSDB; ACA03625.
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05-JAN-2000;
06-JAN-2000;
11-FEB-2000;
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                                                        EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420
                KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLOKYLKSKESVSHAILQTDQAL 480
                         Human; PRO polypeptide; secreted and transmembrane protein;
tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;
differentiation; chondrocyte; tumour; genetic disorder; cytostatic.
                                                                                                                                      ABU66592 standard; protein; 586 AA
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Gao W;

ABUS9673 standard; protein; 586 AA.

ABU59673

(first entry)

13-MAY-2003

ABU59673;

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The present invention relates to the isolation of novel human PRO
polypeptides, and the polynucleotide sequences encoding them. The PRO
polypeptides are secreted and transmembrane proteins. The PRO
polypeptides are secreted and transmembrane proteins. The PRO
polypeptides are useful for detecting other PRO polypeptides, for linking
bloactive molecules to calls expressing PRO polypeptides, for modulating
comparison of calls expressing PRO polypeptides, and for for
identifying agonists or antagonists. The PRO polypeptides are useful for
for stimulating the release of tumour necrosis factor (TNF)-alpha from
thuman blood, for stimulating the proliferation or differentiation of
chondrocytes, and detecting the presence of tumours. The polymucleotide
sequences encoding PRO polypeptides are useful as hybridisation probes,
in chromosome and gene mapping, in the generating fransgenic
DNA, in the preparation of PRO polypeptides for generating transgenic
animals or knockout animals, for the genetic analysis of individuals with
channel PRO polypeptides of the invention. Note: The sequence data for this
patent was obtained in electronic format directly from the USPTO web site
at seqdata.uspto.gov/psipsDIDEntry.html
                       , in chromosome and gene mapping, as chromosome markers, in tissue and in chromosome identification.
secreted and transmembrane PRO nucleic acids, useful for gene
                                                                                                                 Claim 12; Fig 46; 660pp; English.
                             therapy,
                                                              typing,
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Sequence 586 AA;

ö 480 540 540 120 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120 180 LISSTFVYNTVNKI DQGAIDLIANVTELTDLIKARNSPDLDRVEDPADSASFPPDLVWTL 180 240 240 360 360 420 480 HQKKLLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300 9 9 RDFCLGLEIDGGLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 1 MALEIHMSDPMCLIENFNEGLKVNQEALEILSAITQPVVVVAIVGLYRIGKSYLMNKLAG 1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQABEVLQKYLKSKESVSHAILQTDQAL KOGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL **TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ** Gaps ö Length 586; 0; Indels 92.5%; Score 2815; DB 6; I. 100.0%; Pred. No. 1.2e-222; ive 0; Mismatches 0; Best Local Similarity 100. Matches 549; Conservative 549 OKMOEOOMO 549 OKMOEDOMO 19 61 121 181 181 241 241 301 301 361 361 421 421 481 541 Query Match 121 481 g 유 g g 셤 g ઠે 셤 유 ð ò ò à ò ò ò ð ò

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Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing; cardiac insufficiency disorder; cancer; tumour; immune response; adrenal cortical capillary endothelial growth; c.fos induction; endothelial growth factor inhibition; VBGF inhibition; retinal cell growth inhibitor; T-lymphocytes stimulation; retinal neurons cell survival; rod photoreceptor cell survival; retinal disorder; retinitis pigmentosum; kidney disorder; mammalian kidney mesangial cell proliferation; Berger disease; dermatitis; herpetiformis; Crohn's disease; chondrocyte proliferation; chondrocyte redifferentiation; sports injury; arthritis.
                                                           Novel secreted and transmembrane protein PRO4987
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2000WO-US000376.
2000WO-US003565.
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19-DEC-2001; 2001US-00028072
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24-AUG-2000;
08-NOV-2000;
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## (GETH ) GENENTECH INC.

Gao Beresini M, Deforge L, Desnoyers L, Filvaroff E, G IE, Goddard A, Godowski PJ, Gurney AL, Sherwood S; tewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z; Stewart TA, Baker KP, Be Gerritsen ME, Smith V,

## WPI; 2003-148238/14. N-PSDB; ABX89163.

Two hundred and seventy five nucleic acids encoding PRO polypeptides, useful for treating pericyte-associated tumors, diabetes and various bone and/or cartilage disorders, e.g. arthritis. The invention describes an isolated human PRO polypeptide. The PRO polypeptides are useful in detecting PRO polypeptides in a sample, in linking a bioactive molecule to a cell expressing a PRO polypeptide, and Claim 12; Fig 46; 659pp; English

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cc in modulating at least one biological activity of a cell expressing a PRO polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus cusful for treating cardiac insufficiency disorders. PRO1354 and PRO1366 etimulate adrenal cortical capillary endothelial growth, and PRO536, PRO943, PRO943, PRO926, PRO186 or PRO535, PRO943, PRO928, PRO943, PRO926, PRO186 or PRO535, PRO943, PRO928, PRO9186, PRO186 or PRO535, PRO926, PRO919, PRO1126, PRO1367 induce c-fcs in endothelial cells, and are thus useful for treating conditions or disorders where angiogenesis would be beneficial, e.g. wound healing and antagonist of this polypeptide are useful for treating cancerous tumours. PRO812 inhibits vascular colothelial growth factor (VEGP) stimulated proliferation of endothelial cells and is thus useful for inhibiting endothelial cell growth. PRO826, PRO1086, PRO1184, PRO1346 and PRO1375 stimulated proliferation of estimulated T-lymphocytes and are therapeutically useful for enhancing immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of cretinal neurons cells (PRO1132 is also enhances survival/proliferation of colothococeptor cells) and therefore are useful for treating retinal discretes of injuries, e.g. retinitis pigmentosum, AMD. PRO819, PRO813 and PRO11066 induce proliferation of mammalian kidney measagial cells, and therefore associated with dermatitis, herpetiformis or Crohn's decreased measangial cell function such as Berger disease or other cheptorese. PRO1310, PRO844, PRO1312, PRO1192 and PRO110eration and/or redifferentiation of chondrocytes in culture and are thus useful for treating sports injuries, and arthritis. This is the amino acid sequence of a novel human PRO protein 300 360 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180 360 420 540 540 9 1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKKCFIFDLPA RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA HOKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 241 HOKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER EAI EVPWKNS FKDVDQS FQKELETLLDAKQNDI CKRNLEASSDYCSALLKDI FGPLEEAV EAIEVEMKNSFKDVDQSFQKELETILDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER KOGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL Gaps ö Length 586; 0; Indels 92.5%; Score 2815; DB 6; L 100.0%; Pred. No. 1.2e-222; ive 0; Mismatches 0; Matches 549; Conservative 549 Query Match Best Local Similarity OKMOEDOMO Sequence 586 AA; 61 121 j21 181 181 241 301 421 61 301 361 481 361 421 481 541 g ઠે d 셤 ò g g 엄 à 셤 g ð`. g ሯ ઠે Š ò ઠ ò

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Human; PRO; secreted protein; transmembrane protein; tumour; cytostatic; gene therapy; tumour necrosis factor-alpha; TNF-alpha; blood; proteoglycan; cartilage; cytokine; peripheral blood mononuclear cell; PBMC; glucose uptake; FFA; skeletal muscle cell; adipocyte cell; chondrocyte cell proliferation; chondrocyte cell differentiation; pericyte cell; inner ear utricular supporting cell; T-lymphocyte cell; endothelial cell; A-peptide; factor VIA.
                                                                   Human secreted/transmembrane protein (PRO) #23.
                      ABO24863 standard; protein; 586 AA
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06-JAN-2000; 2000WO-US00376.
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13-SEP-1999)
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14-JUL-1998;
28-AUG-1998;
10-SEP-1998;
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The invention relates to an isolated nucleic acid comprising at least 80% sequence identity to a PRO (secreted and transmembrane protein) cDNA comprising a nucleic acid (a) encoding a PRO polypeptide, or its extracellular domain (with or without its associated signal peptide),
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A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
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2000MO-US032678
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2001WO-US06666
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Stewart TA,
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N-PSDB; ACD41817.
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Smith V,
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which comprises any of the 275 120-850 residue amino acid sequences, given in the specification; (b) comprising any of the 275 300-3500 mucleotide sequence of the nucleotide sequences given in the specification; or of the DNA deposited under any of the American Type (Lull-length coding sequence of the nucleotide sequences given in the specification. or of the DNA deposited under any of the American Type (Culture Collection, Or of the DNA deposited under any of the American Type (Culture Collection, or of the DNA deposited under any of the American Type (Comprising the vector, producing a PRO polypeptide, the isolated PRO polypeptide of fused to a heterologous amino acid sequence, an anti-PRO polypeptide of fused to a heterologous amino acid sequence, an anti-PRO polypeptide, modulating a PRO polypeptide in a sample suspected of containing the PRO polypeptide, modulating a bioactive biological activity of a cell expressing a PRO polypeptide, stimulating the prological activity of a cell captor-alpha (TNR-alpha) from human blood (or proteoglycans from cartilage or cytokine from peripheral blood mononclear cells (PBMC)), andipocyte cells (stimulating the proliferation of inner ear utricular supporting cells (or of T-lymphocyte cells, or of endothelial cells), inhibiting the binding of A-peptide to factor VIIA, or differentiation of adipocyte cells (or of T-lymphocyte cells, or of endothelial cells), inhibiting the proliferation of inner ear utricular supporting cells (or of T-lymphocyte cells, or of endothelial cells), inhibiting the proliferation of inner ear utricular supporting cells (or of T-lymphocyte cells, or of endothelial cells), inhibiting the proliferation of inner ear utricular supporting cells detecting the presence of a tumour in a mammal and an oligonucleotide probe derived from any of the nucleotide sequences given in the specification. The polynucleotide is useful in molecular or in the specification. The polynucleotide is useful in molecular or in the mammal swhich, in turn, are useful in the dev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antibody is used in preparing a medicament for treating a condition responsive to the polypeptide or antibody, such as tumours, and in various diagnostic assays. The present sequence rperesents a PRO
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KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120 240 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240 420 480 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180 HOKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360 HOKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300 1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60 EAIEVFWKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL Gaps ö 92.5%; Score 2815; DB 6; Length 586; 100.0%; Pred. No. 1.2e-222; ive 0; Mismatches 0; Indels 0 Query Match Best Local Similarity 100. Matches 549; Conservative 61 61 121 121 181 241 241 301 181 301 361 361 421 421

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         481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ
                                                                                                                                                          inflammatory disease; organ failure; atherosclerosis; cardiac injury; infertility; birth defects; premature aging; AIDS; biosensor; acquired immunodeficiency syndrome; cancer; diabetic complication;
                                                                                                                                   Human secreted/transmembrane, PRO, protein SEQ ID 46.
                                                                                                                                                   Human; secreted protein; transmembrane protein; PRO;
                                                                                   ABU66868 standard; protein; 586
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19-JUN-2001; 2001US-00886342.
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05-APR-2001; 2
10-MAY-2001; 2
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01-JUN-2001; 2
01-JUN-2001; 2
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08-NOV-2000;
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29-JUN-2001;
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Deforge L, Desnoyers L, Filvaroff E, G A, Godowski PJ, Gurney AL, Sherwood S; Tumas D, Watanabe CK, Wood WI, Zhang Z; Beresini M, De ME, Goddard A, Gerritsen ME, Goddard Smith V, Stewart TA, (GETH ) GENENTECH INC. Baker KP,

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New secreted and transmembrane nucleic acids and polypeptides, designated as PRO, useful for treating inflammation, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, or WPI; 2003-331925/31. N-PSDB; ACA04046.

480

KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL

421

The invention relates to an isolated nucleic acid comprising, or which is at least 80% identical to, or the full-length coding sequence of, any of the 275 nucleotide sequences, encoding the corresponding PRO polypeptide (one of 275 secreted or transmembrane proteins). The nucleic acid further comprises the full-length coding sequence of the DNA deposited under American Type Culture Collection (ATCC) accession number in a list given in the specification. Also included are vectors and host cells for producing PRO proteins, PRO fusion proteins, anti-PRO antibodies, PRO extracellular domains and mature sequences, methods of detecting PRO proteins, methods for stimulating the release of TMF-alpha (tumour necrosis factor alpha) from human blood, (and the proliferation of chondrocyte cells, the proliferation of chondrocyte cells, the release or proteeglycans from expression in pericyte cells, the release or proteeglycans from cartilage, proliferation of T-lymphocyte cells, the release or a cytokine from peripheral blood mononuclear cells, the release of a cytokine from peripheral blood mononuclear cells, the release of a cytokine from peripheral blood mononuclear cells, method for modulating the uptake of glucose or free cartilage, proliferation of factor villa, or the differentiation of adjocotte cells, a method for detecting the presence of a tumour in a mammal and an olinding of A-peptide to factor villa, or the differentiation of adjocotte cells, and the proliferation of adjocotte cells, and polypeptides are useful for treating and polypeptides are useful for treating infertility, birth defects, premature adjng, AIDS (acquired immunodeficiency syndrome), cancer, or diabetic complications and gene useful as pharmaceuticals, diagnostics, biosensors or bioreactors. Both cuells as pharmaceuticals, diagnostics, biosensors or bioreactors. Both are useful in tissue typing. The present sequence represents a PRO protein of the invention ö 61 KANKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120 9 1 MALBIHMSDPMCLIENFNEQLKVNQBALBILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL Gaps .; 0 92.5%; Score 2815; DB 6; Length 586; 100.0%; Pred. No. 1.2e-222; ive 0; Mismatches 0; Indels ( Claim 12; Fig 46; 659pp; English. Local Similarity 100. Sequence 586 AA; 61 Query Match Best Loca Matches a ò g 8

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                  241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300
LLESTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180
                                                                                                 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360
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                                                                            RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA
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Novel secreted and transmembrane polypeptide for modulating biological
99WO-US030999.
99WO-US030720.
99WO-US031274.
99WO-US031274.
2000WO-US000219.
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2000WO-US034956.
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2000WO-US022031
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2000WO-US030873
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06-JAN-2000;
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11-FEB-2000;
18-FEB-2000;
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22-FEB-2000;
24-FEB-2000;
24-FEB-2000;
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18-MAY-2001;
25-MAY-2001;
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21-JUN-2001;
22-JUN-2001;
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08-NOV-2000;
10-NOV-2000;
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11-AUG-2000;
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22-MAR-2001;
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25-MAY-2001;
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 Human; secreted and transmembrane protein; PRO;
Tumour necrosis factor alpha release; TNF-alpha release;
glucose uptake modulator;
cell proliferation etimulator; cell differentiation stimulator;
cell differentiation inhibitor; cytokine release stimulator; tumour;
lung tumoue; colon tumour; breast tumour; prostate tumour; rectal tumour;
cervical tumour; liver tumour; chromosome mapping; gene mapping;
gene therapy; chromosome identification; chromosome marker.
Novel human secreted and transmembrane protein PRO4987
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                                                                                    ADA45565 standard; protein; 586
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99WO-US000106
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                              OKMOEQOMO 549
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01-DEC-1998;
05-JAN-1999;
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07-OCT-1998;
29-OCT-1998;
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Gao W; Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, G Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z; 2001US-00874503. 2001US-00882636. 2001US-00886342. 2001WO-US006666 2001US-00802706 2001US-00808689 2001US-00816744 2001US-00854208 2001US-00854280 2001US-00860216 2001US-00866028 2001US-00866034 2001WO-US017800 2001WO-US019692 2001US-00887879 16-AUG-2001; 2001US-00931836 19-DEC-2001; 2001US-00028072 2001US-00828366 2001WO-US017092 2001WO-US021735 2001WO-US020116 2001WO-US021066 2001US-00924419 2001US-00927796 (GETH ) GENENTECH INC. WPI; 2003-584997/55. N-PSDB; ADA45564.

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                                                                                                                                                                         transmembrane) polypeptides (1). (1) is useful for stimulating the transmembrane) polypeptides (1). (1) is useful for stimulating the release of TNF-alpha from human blood, for modulating the uptake of release of TNF-alpha from human blood, for modulating the uptake of glucose or FFA by skeletal muscle cells or adjocyte cells, for stimulating the proliferation of or gene expression in pericyte cells, for stimulating the proliferation of or gene expression in pericyte cells, for stimulating the proliferation of or gene expression in pericyte cells, for stimulating the proliferation of nor T-lymphocyte cells, for stimulating of the release of profesolycans from cartilage, for stimulating the proliferation of nor T-lymphocyte cells, for stimulating of A-peptide to factor VIIA, for inhibiting the differentiation of adipocyte cells, for stimulating proliferation of endothelial cells, for detecting the presence of tumour in a mammal. The tumour is lung, colon, breast, cretal, cervical or liver tumour. The oligomuclectide probes are useful for isolating genomic and cDNA nuclectide sequences or antisense probes. (1) is also useful as therapeutic agent. PRO is useful in the cand gene mapping, in generation of antisense RNA and DNA, in the creation of PRO polypeptide, for generating transgenic animals which in turn are useful in the development and creaming of therapeutically useful reagents, in gene therapy, for chromosome identification, as chromosome marker, and for generating trobbes. An anti-(1)-antibody is useful in diagnostic assays for PRO, enchonomic of an antification of PRO properties or serum, and for generating its expression in specific cells, tissues or serum, and for colling typurification of PRO from recombinant cell culture or natural colling typurification of PRO from recombinant cell culture or natural colling the sequence of a novel human secreted and transmembrane PRO
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activity of cell expressing the polypeptide, identifying agonists antagonists of polypeptide, and as molecular weight markers.
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                                                                                                  Claim 12; Fig 46; 659pp; English.
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            Human; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; FFA; skeletal muscle cell; adipocyte cell; pericyte cell; inner ear utricular supporting cell; T-lymphocyte cell; endothelial cell tube formation; bone disorder; cartilage disorder; sports injury; proteoglycan; articular cartilage defect; osteoarthritis; rheumatoid arthritis; haemoglobin-associated disorder thalassaemia; immune system cell infiltration.
481 TETEKKKKBAQVKABABKABAQRLAAIQRQNBQMMQBRBRLHQEQVRQMBIAKQNWLABQ
                                                                                                                       ADA75996 standard; protein; 586 AA.
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99WO-US010733.
99WO-US012252.
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99WO-US028564.
99WO-US028565.
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                                                                                                                                                                 (first entry)
                                                                                                                                                                                     Human PRO polypeptide #23
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10-MAR-1999;
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14-MAY-1999;
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05-OCT-1999;
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ADA75996
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99WO-US030095.
99WO-US030911.
99WO-US030999.
99WO-US031243.
                       99WO-US031274.
2000WO-US000219.
2000WO-US000277.
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06-JAN-2000;
06-JAN-2000;
11-PEB-2000;
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25-MAY-2001;
25-MAY-2001;
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28-FEB-2001;
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(GETH ) GENENTECH INC.

Gao W; Deforge L, Desnoyers L, Filvaroff E, G A, Godowski PJ, Gurney AL, Sherwood S; Lumas D, Watanabe CK, Wood WI, Zhang Z; Baker KP, Beresini M, Deforge I Gerritsen ME, Goddard A, Godowi Smith V, Stewart TA, Tumas D,

2003-687639/65 WPI; 2003-687639/ N-PSDB; ADA75995

420

EAIEVFWKONS FKDVDQS FQKELETILLDAKQNDICKRNLEASSDYCSALLKDI FGPLEEAV

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The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO invention also relates to an antibody which specifically binds to a PRO invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis a factor-alpha (TNF-alpha) from human blood, a method for stimulating the presence of a tumour in a mammal (e.g. adrenal, lung, colon, breast, prostate, rectal, kidney, cervical and liver tumours). The prolynucleotides are useful in molecular biology, in generating a colon, breast, prostate, rectal, kidney, cervical and liver tumours). The polynucleotides may also a trisense RNA and BNA and in gene therapy. The polynucleotides may also a trisense RNA and BNA and in gene therapy. The polynucleotides may also be used in preparing PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the development and screening of knock-out animals which are useful in the development and screening of knock-out animals which are useful in the development and screening of knock-out animals which are useful an tenderhelial cells, for modulating the uptake of cluman microvascular muscle cells or adipocyte cells, for stimulating differentiation of adipocyte cells, for stimulating the proliferation of orgene expression in pericyte cells, for stimulating the proliferation of funer ear utricular supporting cells or T-lymphocyte cells, for medicanting endothelial cell tube formation and for treating articular cartilage are useful for treating sports endiated joint problems articular cartilage are useful for treating sports related joint problems articular cartilage are useful for treating sports related joint problems associated disorders such as various thalassasemias and condition. This sequence teps are useful as also aveined in electric time. New isolated nucleic acid encoding a secreted and transmembrane polypeptide, designated e.g. PRO1114 or PRO4978, useful in chromosome and gene mapping, in generating antisense RNA and DNA, and in gene therapy. Claim 12; Fig 46; 659pp; English 

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180 240 240 9 1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL RDFCLGLEIDGQLVTPDEXLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA HOKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN HQKKLAQLETLPDDELEPBEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG KNKGPSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER Gaps ô Length 586; 92.5%; Score 2815; DB 6; Length 5 100.0%; Pred. No. 1.2e-222; ive 0; Mismatches 0; Indels Best Local Similarity 100. Matches 549; Conservative 241 ] 61 121 181 301 181 Query Match 241

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EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420
                                                                                                                                                    Human; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; lung; colon; breast; prostate; rectum; cervix; liver; tumour; cancer; glucose uptake, FFA; adipocyte cell; pericyte cell; proteoglycan; cartilage; inner ear utricular supporting cell; cytokine; A-peptide; factor VIIA; endothelial cell.
           ADA18646 standard; protein; 586 AA
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98WO-US018824.
98WO-US019093.
98WO-US019094.
98WO-US019177.
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99WO-US028551
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12-JUN-1998;
28-AUG-1998;
10-SEP-1998;
14-SEP-1998;
14-SEP-1998;
16-SEP-1998;
17-SEP-1998;
07-OCT-1998;
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29-OCT-1998;
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20-APR-1999;
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Deforge L, Desnoyers L, Filvaroff E, Ga
A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
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2000US-00747259.
2000WO-US034956.
2001US-00796498.
2001WO-US006520.
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2001US-00802706
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2001US-0081244
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20010G-00882636.
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2000MO-US005746.
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2000WO-US008439.
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2000WO-US020710.
2000WO-US022031.
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2001US-00887879.
2001WO-US020116.
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2001US-00931836
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Gerritsen ME, Goddard
Smith V, Stewart TA,
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19-JUN-2001;
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06-JAN-2000;
11-FEB-2000;
11-FEB-2000;
18-FEB-2000;
24-FEB-2000;
24-FEB-2000;
24-FEB-2000;
01-MAR-2000;
02-MAR-2000;
01-MAR-2000;
10-MAR-2000;
11-MAR-2000;
30-MAR-2000;
30-MAR-2000;
31-MAR-2000;
02-DEC-1999;
16-DEC-1999;
20-DEC-1999;
22-DEC-1999;
30-DEC-1999;
30-DEC-1999;
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11-AUG-2000;
23-AUG-2000;
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06-AUG-2001;
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19-DEC-2001;
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05-APR-2001;
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08-NOV-2000;
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Gao W;

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ADA61269 standard; protein; 586 AA
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                                                                                                                                                                                                                                                     The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polymucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNP-alpha) from human blood, a method for stimulating the proliferation or differentiation of chondrocyte cells and a method for checting the presence of a tumour in amammal (e.g. lung, colon, breast, prostate, rectal, cervical and liver tumours). The polymucleotides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and bnA and in gene therapy. The polymucleotides may also be used in preparing PRO polypeptides by recombinant techniques and in generating either cransgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful reagents. The PRO polypeptides or antibodies are used in preparing a medicament for traating a condition responsive to the polypeptides or antibodies, such as tumours, for modulating the uptake of glucose or PRA by adipocyte cells, for stimulating the proliferation of or gene expression in pericyte cells, for stimulating the proliferation of inner ear utricular capporting cells, for stimulating the proliferation of cytokines from PRO cartilage, for stimulating the proliferation of cytokines from PRO catilage, for inhibiting the binding of A-peptide to factor VIIA, for similating the binding of A-peptide to factor viia patent is proliferation. Note: The sequence represents a human PRO polypeptide of the invention. Note: The sequence data for this patent is also available in electronic format from USPTO at
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                                                      PRO nucleic acid, useful for preparing a composition for treating
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                                                                                                                Claim 12; Fig 46; 660pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0
Matches 549; Conservative
2003-521854/49.
                  N-PSDB; ADA18645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 586 AA;
                                                                              e.g., tumors
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481 TETEKKKKEAQVXAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540
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glucose uptake modulator; FFA uptake modulator;
cell proliferation stimulator; cell differentiation stimulator;
cell differentiation inhibitor; cytokine release stimulator; tumour;
lung tumoue; colon tumour; breast tumour; prostate tumour; rectal tumour;
cervical tumour; liver tumour; chromosome mapping; gene mapping;
gene therapy; chromosome identification; chromosome marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, secreted and transmembrane protein; PRO;
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The invention describes 305 nucleic acids encoding PRO (secreted and transmembrane) polypeptides (I). (I) is useful for stimulating the cransmembrane) polypeptides (I). (I) is useful for stimulating the profile from human blood, for modulating the uptake of glucose or FPA by skeletal muscle cells or adipocyte cells, for glucose or FPA by skeletal muscle cells or adipocyte cells, for stimulating the proliferation of or gene expression in perioryte cells, for stimulating the proliferation of inner ear utricular supporting cells, cor stimulating the proliferation of funcer ear utricular supporting cells, cor stimulating the proliferation of for the release of a cytokine from PBMC cells, for stimulating the proliferation of endothelial cells, for stimulating the proliferation of endothelial cells, for detecting the presence of tumour in a mammal. The tumour is lung, colon, breast, colls, for stimulating proliferation of endothelial cells, for detecting the presence of tumour in a mammal. The tumour is lung, colon, breast, corostate, rectal, cervical or liver tumour. The oligonuclectide probes are useful for isolating genomic and cDNA nuclectide sequences or antisense probes. (I) is also useful as therapeutic agent. PRO is useful in assays to identify other proteins or molecules involved in binding interaction. A polynuclectide (II) encoding (I) is useful in chromosome corome identification of antisense RNA and DNA, in the preparation of PRO polypeptide, for generating transgenic animals which in turn are useful in the development and corremance in mains which in turn are useful in diagnostic assays for PRO, correcting its expression in appendict cells, tissues or serum, and for affinity purification as chromosome marker, and for generating correcting its expression in appendict cells, tissues or serum.

Correcting its expression in procession of transmembrane PRO
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  A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
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                                                                                                                                        New PRO nucleic acid and encode polypeptides, are useful for manufacturing a medicament for diagnosing or treating cancer.
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                                                                                                                                                                                                                    Claim 12; Fig 46; 660pp; English.
Goddard A,
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4atches 549; Conservative
                             Stewart TA,
                                                                         WPI; 2003-695892/66.
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                                                                                                 N-PSDB; ADA61268
       Gerritsen ME,
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99WO-US030095.
99WO-US030911.
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Gao W;

Beresini M, Deforge L, Desnoyers L, Filvaroff E,

Baker KP,

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Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gr
Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
                                   99WO-US030999.
99WO-US030720.
99WO-US031243.
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22-MAY-2000
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                                                                 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540
                                                                              361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420
                                     421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480
                      KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL
                                                                                                                                                                                                                                                                                  Human; secreted and transmembrane protein; PRO;
Tumour necrosis factor alpha release; TNF-alpha release;
glucose uptake modulator; FPA uptake modulator;
cell proliferation stimulator; cell differentiation stimulator;
cell differentiation inihibitor; cytokine releas.
                                                                                                                                                                                                                                                             Novel human secreted and transmembrane protein PRO4987
                                                                                                                                                                                          ADB19054 standard; protein; 586 AA
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99WO-US010733.
99WO-US012252.
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14-SEP-1998;
16-SEP-1998;
17-SEP-1998;
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Query Match 92.5
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                   il secreted and transmembrane PRO polypeptides useful for stimulating release of tumor necrosis factor alpha and detecting the presence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, PRO, secreted polypeptide, transmembrane polypeptide;
tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour;
cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix;
                                                                                                                                                                                                                MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG
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                                                                                                                                                                             Gaps
                                                                               The invention describes 305 nucleic acids encoding PRO (secreted and transmembrane) polypeptides (I). (I) is useful for stimulating the release of TNF-alpha from human blood, for modulating the uptake of glucose or PRA by skeleral muscle cells or adipocyt
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                                                                                                                                                        Length 586;
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                                                                                                                                                        92.5%; Score 2815; DB 6; L 100.0%; Pred. No. 1.2e-222; ive 0; Mismatches 0;
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                                                             Claim 12; Fig 46; 660pp; English.
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                                         tumor in a mammal.
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N-PSDB; ADB19053
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Matches 549;
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The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polymucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, a method for stimulating the proliferation or differentiation of chondrocyte cells and a method for colon, breast, prostate, rectal, kidney, cervical and liver tumours). The colon, breast, prostate, rectal, kidney, cervical and liver tumours). The colon, breast, prostate, rectal, kidney, cervical and liver tumours). The colon, breast, prostate, in chromosome and gene mapping, in generating antisense RNA and DNA and in gene therapy. The polymucleotides may also contisense RNA and DNA and in gene therapy. The polymucleotides may also be useful in the development and screening of therapeutically useful caparing BNO polypeptides by recombinant techniques and in generating ether transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful caparing a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of human microvascular endothelial cells, for adipocyte cells, for stimulating differentiation of adipocyte cells, for stimulating colliferation of inner ear utricular supporting cells for reating cells, for reating endothelial cell tube formation and for treating cells, for warious bone and/or cartilage disorders such as sports injunyered various continues and continues and prometice and utricular supporting cells, for warious pone and/or cartilage disorders such as sports injunyeries and various continues and primer expression in pericyte cells, for when and we have an utricular such as sports for proliferating or remaining the formation of inner expression in pericyte cells, for proprime warious and profere expression in pericyte cells, for proprime warious and pericular cells, 
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liver; microvascular endothelial cell; glucose; FFA; skeletal muscle cell; adipocyte cell; pericyte cell; inner ear utricular supporting cell; T-lymphocyte cell; endothelial cell tube formation; bone disorder; cartilage disorder; sports injury; proteoglycan; articular cartilage defect; osteoarthritis; rheumatoid arthritis; haemoglobin-associated disorder thalassaemia; immune system cell infiltration.
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01-DEC-2000; 2000WO-US032678.
19-DEC-2001; 2001US-00028072.
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ME, Goddard
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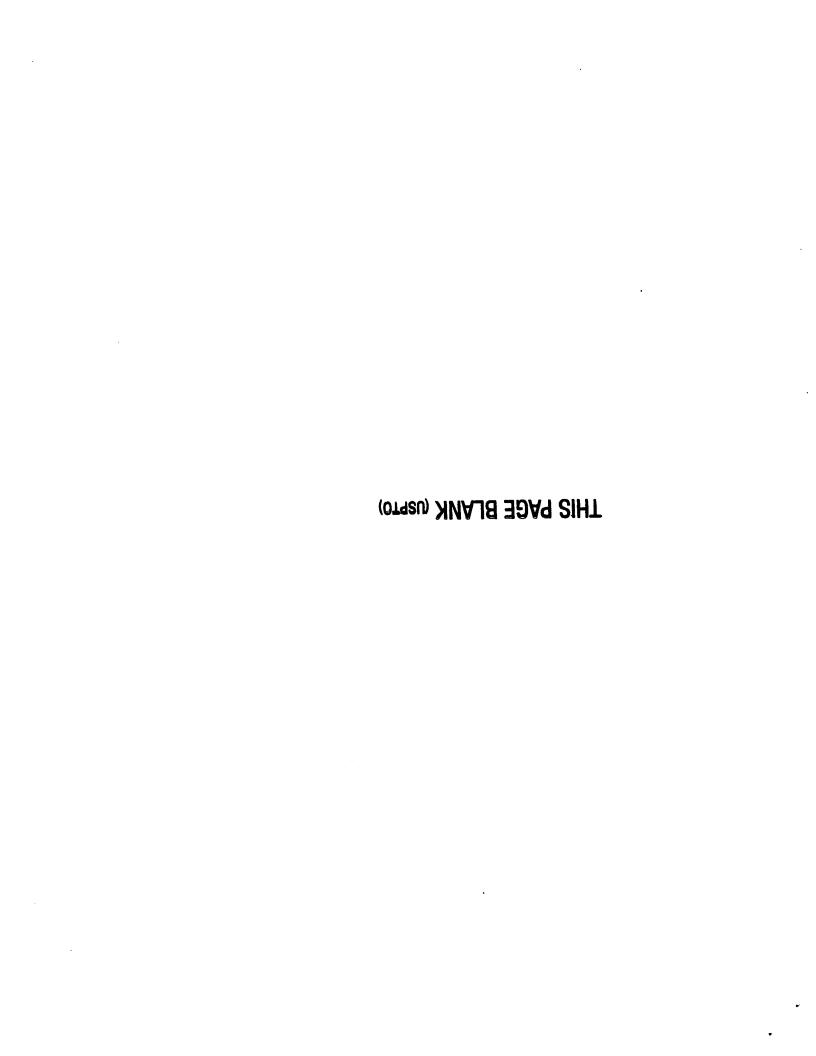
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Length 586; Indels

92.5%; Score 2815; DB 6; I 100.0%; Pred. No. 1.2e-222;

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KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL
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Title: Perfect

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Run on:

Scoring table:

Total number

Database

Searched:

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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: 1BM PC compatible COMPUTER: 1BM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATH:
APPLICATION NUMBER: US/10/659,549 FILING DATE: 10-Sep-2003 CLASSIFICATION A15
PRIOR APPLICATION DATA:
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Sequence 3, Application US/10659549

Publication No. US20040229307A1

GENERAL INFORMATION:

APPLICANT: Diane Pennica

TITLE OF INVENTION: GUANYLATE-BINDING PROTEIN

NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CTTY: South San Francisco

STATE: CALlifornia

COUNTRY: USA
                      US-10-143-114-46
US-10-142-419-46
US-10-142-419-46
US-10-142-423-46
US-10-141-755-46
US-10-141-755-46
US-10-141-755-46
US-10-123-218-46
US-10-123-218-46
US-10-123-218-46
US-10-123-292-46
US-10-124-928-46
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US-10-131-939A-46
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REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1056
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/252-1896
TELEFAX: 650/952-9881
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1409.390 Million cell updates/sec
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| cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.ppp:*
| cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.ppp:*
| cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.ppp:*
| cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.ppp:*
| cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.ppp:*
| cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.ppp:*
| cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.ppp:*
| cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.ppp:*
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| cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.ppp:*
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| cgn2_6/ptodata/2/pubpaa/USO09_PUBCOMB.ppp:*
| cgn2_6/ptodata/2/pubpaa/USO09_PUBC
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                      GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-028-072-46
US-10-121-0808-46
US-10-123-904-46
US-10-123-904-6
US-10-175-746-46
US-10-176-918-46
US-10-176-918-46
US-10-176-918-46
US-10-176-918-46
US-10-137-865-46
US-10-137-865-46
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                protein search, using sw model
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                                                                                                                       Length 591;
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                                                                                                                     100.0%; Score 3043; DB 16;
100.0%; Pred. No. 2.3e-213;
ive 0; Mismatches 0;
                                                            TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 2
US-10-028-072-46
; Sequence 46, Application US/10028072
; Publication No. US20030004311A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 591 amino acida
TYPE: Amino Acid
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Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K
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Gerritsen, Mary E.
Goddard, Audrey
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Gurney, Austin L.
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Filvaroff, Ellen
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Best Local Similarity 100.
Matches 591, Conservative
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TITLE OF INVENTION:

PILE REPRENCE:
CURRENT APPLICATION NUMBER: US/10/28,072
CURRENT APPLICATION NUMBER: 60/64911
PRIOR PILLING DATE: 1997-06-18
PRIOR PILLING DATE: 1997-06-19
PRIOR PILLING DATE: 1997-06-19
PRIOR PILLING DATE: 1997-09-17
PRIOR PILLING DATE: 1997-09-17
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R APPLICATION NUMBER: 60/073612

R FILING DATE: 1998-02-04

R FILING DATE: 1998-02-09

R APPLICATION NUMBER: 60/074086

R APPLICATION NUMBER: 60/074092

R APPLICATION NUMBER: 60/07791

R FILING DATE: 1998-02-09

R APPLICATION NUMBER: 60/07791

R APPLICATION NUMBER: 60/079910

R APPLICATION NUMBER: 60/079294

R FILING DATE: 1998-03-25

R APPLICATION NUMBER: 60/079663

R APPLICATION NUMBER: 60/079663

R APPLICATION NUMBER: 60/079683

R FILING DATE: 1998-03-27

R APPLICATION NUMBER: 60/081203

R R PILING DATE: 1998-04-09
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DR APPLICATION NUMBER: 60/081818

DR APPLICATION NUMBER: 60/081918

R PILING DATE: 1998-04-15

DR APPLICATION NUMBER: 60/081322

R FILING DATE: 1998-04-24

PRILING DATE: 1998-04-28

R PILING DATE: 1998-04-28

DR APPLICATION NUMBER: 60/08345

R PILING DATE: 1998-04-29

DR APPLICATION NUMBER: 60/084600

R FILING DATE: 1998-05-07

R APPLICATION NUMBER: 60/084627

R PILING DATE: 1998-05-07

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R PELLING DATE: 1997-12-11

R PELLING DATE: 1997-12-11

R APPLICATION NUMBER: 60/069694

R PILING DATE: 1997-12-16

R APPLICATION NUMBER: 60/072320

R PILING DATE: 1998-01-23
                           FILING DATE: 1997-11-24
APPLICATION WHBER: 60/066770
ALEING DATE: 1997-11-24
APPLICATION NUMBER: 60/069212
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APPLICATION NUMBER: 60/085704
FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/086414
FILING DATE: 1998-05-22
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APPLICATION NUMBER: 60/069278
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FILING DATE: 1998-04-14
APPLICATION NUMBER: 60/081817
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FILING DATE: 1998-05-12
APPLICATION NUMBER: 60/085323
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APPLICATION NUMBER: 60/085338
FILING DATE: 1998-05-13
APPLICATION NUMBER: 60/085339
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APPLICATION UNMBER: 60/085579
FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/085697
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APPLICATION NUMBER: 60/088026
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088730
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APPLICATION NUMBER: 60/088741
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APPLICATION NUMBER: 60/088810 FILING DATE: 1998-07-01
APPLICATION NUMBER: 60/091519
FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/091982
FILING DATE: 1998-07-07 APPLICATION NUMBER: 60/090863 FILING DATE: 1998-06-26 APPLICATION NUMBER: 60/091360 Query Match Best Local Similarity 100. Matches 549; Conservative 361 61 121 181 241 361 301 421 8 유 ઠે ઠે 셤 ઠે 셤 장- 원 δ

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MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330011C17
CURRENT APPLICATION NUMBER: US/10/121,049
CURRENT FILING DATE: 2002-04-12
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NUMBER OF SEQ ID NOS: 550
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llarity 100.0%; Pred. No. 9.9e-197;
Conservative 0; Mismatches 0;
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Publication No. US20030022239A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stewart, Timothy A
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Gerritsen, Mary E.
Goddard, Audrey
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APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
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Wood, William
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Smith, Victoria
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Filvaroff, Ellen
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Matches 549; Conserv
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     APPLICANT: Sherwood, Steven
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Wetanabe, Colin K
APPLICANT: Wood, William
APPLICANT: And SCRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P3330R1C182
CURRENT APPLICANT: 2002-05-07
CURRENT PAPPLICATION NUMBER: US/10/140,808
CURRENT PAPPLOICATION TOWNES: 2002-05-07
Prior Apploication removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
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Publication No. US20030017563A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                       Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
Stewart, Timothy A.
Tumas, Daniel
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Goddard, Audrey
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Filvaroff, Ellen
Gao, Wei-Qiang
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ORGANISM: Homo Sapien
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                                                                                HOKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN
                                                                                                                                                                                                                                                                                                 APPLICANT: TOWARD, THE APPLICANT: TOWARD, THE APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Wood, William
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P3330410160
CURRENT APPLICATION NUMBER: US/10/140,470
CURRENT APPLICATION NUMBER: US/10/140,470
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
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"Sequence 46, Application US/10140470
"Publication No. US20030022331A1
"GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
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Stewart, Timothy A.
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APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
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Filvaroff, Ellen
Gao, Wei-Qiang
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CORGANISM: Homo Sapien
US-10-140-470-46
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C54
CURRENT APPLICATION NUMBER: US/10/123,904
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                               AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER
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100.0%; Pred. No. 9.9e-197;
ive 0; Mismatches 0;
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Prior Application removed - See File Wrapper or
NUMBER OF SEQ ID NOS: 550
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 46, Application US/10123904
Publication No. US20030022328A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
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Goddard, Audrey
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Wood, William
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Gurney, Austin L.
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Filvaroff, Ellen
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Smith, Victoria
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Best Local Similarity 100.
Matches 549; Conservative
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Pred. No. 9.9e-197;

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Best Local Similarity 100.
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APPLICANT: Sherwood, Steven
APPLICANT: Sherwood, Steven
APPLICANT: Sherwood, Steven
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Watanabe, Colin K
APPLICANT: Mananaman SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P3330R1C353
CURRENT APPLICATION NUMBER: US/10/175,746
CURRENT PILING DATE: 2002-06-19
                                                                                                                                                                                          241 HOKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN
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       KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL
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US-10-175-746-46
Selection US/10175746
Publication No. US20030027270A1
GENERAL INFORMATION:
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Flyaroff, Ellen
Gao, Wei-Giang
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Peul J.
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DeForge, Laura
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APPLICANT: Beresini, Mauree,
APPLICANT: DeForge, Laura
APPLICANT: Pilvaroff, Ellen
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary J
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
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LENGTH: 586
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92.5%; Score 2815; DB 14; Length 586;

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APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C382
CURRENT APPLICATION NUMBER: US/10/176, 918
CURRENT FILING DATE: 2002-06-20
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
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Publication No. US20030027275A1
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APPLICANT: Bacer, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeBnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Glang
APPLICANT: Gao, Wei-Glang
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Austin L.
APPLICANT: Steven
APPLICANT: Steven
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Wacanab, Colin K
APPLICANT: Wacanab, Colin K
APPLICANT: Wacanab, Colin K
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLBIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P330MIC288

CURRENT APPLICATION NUMBER: US/10/176,921

CURRENT FILING DATE: 2002-06-20

Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 550

LENGTH: 586
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100.0%; Pred. No. 9.9e-197;
iive 0; Mismatches 0;
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APPLICANT: Beresini, Maureen APPLICANT: DeForge, Laura APPLICANT: Desnoyers, Luc APPLICANT: Filvaroff, Ellen APPLICANT: Gao, Wei-Qiang APPLICANT: Geritsen, Mary E. APPLICANT: Goddard, Audrey APPLICANT: Goddwski, Paul J. APPLICANT: Gurney, Austin L.
                                                                                                                                                                                                                                               Query Match 92.5
Best Local Similarity 100.
Matches 549; Conservative
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US-10-176-921-46
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Publication No. US20030027276A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Deforge, Laura
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Oiang
APPLICANT: Goodwar, Mary E.
APPLICANT: Goodwar, Parkey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Austin U.
APPLICANT: Sherwood, Steven
APPLICANT: Sherwood, Steven
APPLICANT: Stewart, Timochy A.
APPLICANT: Tumas, Daniel
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                                 TYPE: PRT
ORGANISM: Homo Sapien
US-10-176-918-46
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 SEQ ID NO 46
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       APPLICANT: Smith, Victoria
APPLICANT: Tunas, Daniel
APPLICANT: Tunas, Daniel
APPLICANT: Tunas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C154
CURRENT APPLICATION NUMBER: US/10/137, 865
CURRENT FILING DATE: 2002-05-03
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 46
LENGTH: S86
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                                                                                                                                                                                                                                                                                                   Length 586;
                                                                                                                                                                                                                                                                                                                           0, Indels
                                                                                                                                                                                                                                                                                              Query Match 92.5%; Score 2815; DB 14;
Best Local Similarity 100.0%; Pred. No. 9.9e-197;
Matches 549; Conservative 0; Mismatches 0;
Sherwood, Steven
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                                                                                                                                                                                                                                      TYPE: PRT
CORGANISM: Homo Sapien
US-10-137-865-46
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APPLICANT: Gao, Wei-Qiang
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APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Stewart, Timochy
APPLICANT: Stewart, Timochy
APPLICANT: Tumas, Daniel
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APPLICANT: Watanabe, Colin K
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100.0%; Pred. No. 9.9e-197;
iive 0; Mismatches 0;
Desnoyers, Luc
Filvaroff, Ellen
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Best Local Similarity 100.0
Matches 549; Conservative
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ORGANISM: Homo Sapien
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US-10-140-474-46
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RESULT

US-10-140-474-46

Sequence 46, Application US/10140474

Publication No. US20030032156A1

GENERAL INFORMATION:
APPLICANT: Barker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura

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61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG
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                                                                                                                                   Sequence 46, Application US/10143114
Publication No. US20030036180A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         Stewart, Timothy A
                                                                                                                                                                                                                                          DeForge, Laura
Desnoyers, Luc
Filvaroff, Ellen
Gao, Wei-Qiang
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Wood, William
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                                                                                                                                                                                                                                                                                                                                         Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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Best Local Similarity 100.
Matches 549; Conservative
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      OKMOEDOMO 549
                                         541 ÇKMÇEÇÇMÇ 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tumas, Daniel
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ORGANISM: Homo Sapien
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C251
CURRENT APPLICATION NUMBER: US/10/142,431
CURRENT FILING DATE: 2002-05-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 46
LENGTH: 586
TYPE: PRT
ORGANISM: Homo Sapien
Sequence 46, Application US/10142431
Publication No. US20030036179A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                   Stewart, Timothy A
                                                                                                                                                                            Gerritsen, Mary E.
Goddard, Audrey
                                                                                                                                                                                                                                                                                                                    Tumas, Daniel
Watanabe, Colin K
Wood, William
                                                                                Beresini, Maureen
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Gurney, Austin L.
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Filvaroff, Ellen
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                                                                                                  DeForge, Laura
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                                                           APPLICANT: Baker, Kevin P.
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APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SCREETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P3330R1C38
CURRENT APPLICATION NUMBER: US/10/123, 262
CURRENT APPLICATION NUMBER: US/10/123, 262
CURRENT APPLICATION NUMBER: US/10/123, 262
FILE APPLICATION NUMBER: US/10/123, 262
CURRENT APPLICATION NUMBER: US/10/123, 262
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CURRENT APPLICATION NUMBER: US/10/123, 262
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100.0%; Pred. No. 9.9e-197;
ive 0; Mismatches 0;
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Filvaroff, Ellen
Gao, Wei-Qiang
Gerriteen, Mary B.
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Yictoria
Stewart, Timothy A.
Tumas, Daniel
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DeForge, Laura
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Best Local Similarity 100.
Matches 549; Conservative
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ORGANISM: Homo Sapien
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US-10-123-262-46.
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APPLICANT: Gao, Wei-Oiang
APPLICANT: Gao, Wei-Oiang
APPLICANT: Gao, Wei-Oiang
APPLICANT: Gao, Wei-Oiang
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Daniel
APPLICANT: Stewart, Audrenabe, Colin K
APPLICANT: Applicant
APPLICANT: Stewart, Audrenabe, Colin K
APPLICANT: Abang, Zemin
APPLICANT: Abang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C244
CURRENT APPLICATION NUMBER: US/10/142,419
CURRENT FILING DATE: 2002-05-10
Prior Apploication removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NOS: 550
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                                                                                        TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540
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        KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEBVLQKYLKSKESVSHAILQTDQAL 480
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                              481 TETEKKKKEAQVKAEAAGKLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ
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100.0%; Pred. No. 9.9e-197;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                     ; Sequence 46, Application US/10142419; Publication No. US20030044945A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                Desnoyers, Luc
Filvaroff, Ellen
Gao, Wei-Qiang
Gerritsen, Mary E.
Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                           Beresini, Maureen
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Best Local Similarity 100.
Matches 549; Conservative
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; ORGANISM: Homo Sapien
US-10-142-419-46
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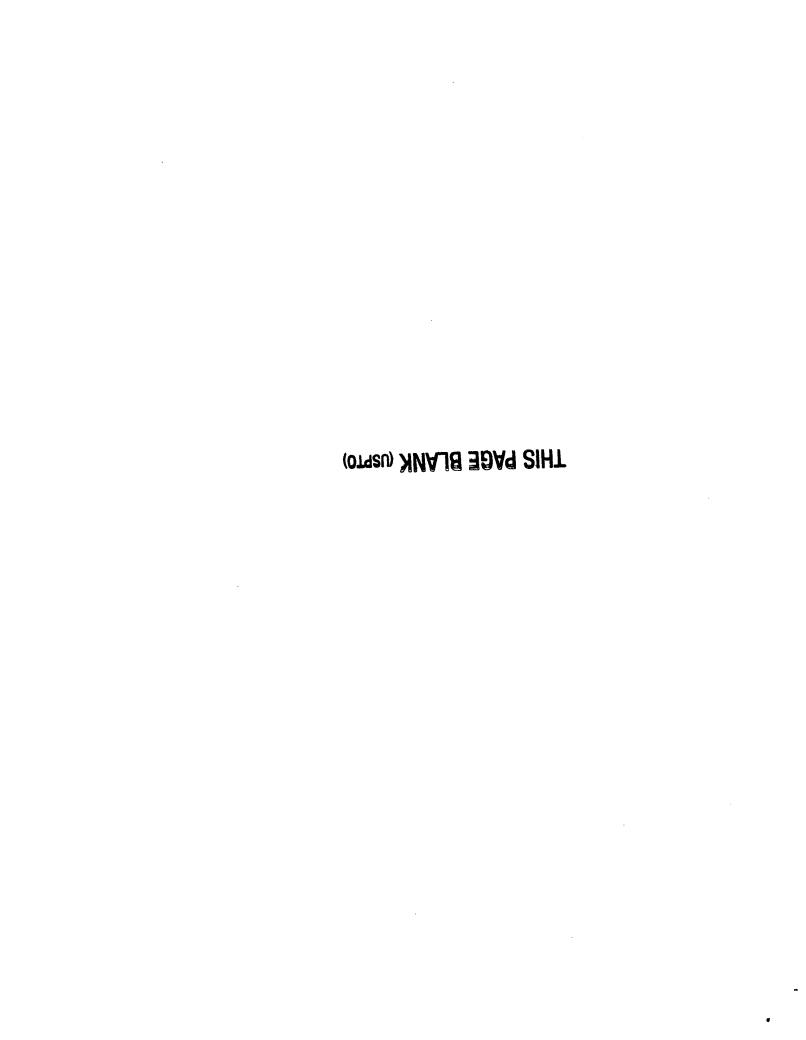
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Search completed: July 9, 2005, 13:41:36 Job time : 164 secs



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GenCore version 5.1.6

Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 9, 2005, 13:15:14 ; Search time 168 Seconds

(without alignments)
1360.568 Million cell updates/sec
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	<pre>(without alignments) 1360.568 Million cell updates/sec</pre>
Title:	US-10-659-549-3
Sequence:	3043 1 MALEIHMSDPMCLIENFNEQGEAARSCGSQQGVWSQKVWV 591
Scoring table: BLOSUM62 Gapop 10	BLOSUM62 Gapop 10.0 , Gapext 0.5
Searched:	2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 200000000

2105692

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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lon	Human g		Human t	Novel h	Human P	Human Pi		Human s	Human B	Novel h		Human P	Homo sapi	Novel h	Human P		Human P	Human P	Human P	Human P	Novel h	Human P	_	Novel h	Human Pl
Description	Add95076	Aau12194	Abb77445	Abo17638	Abu80892	Abu66592	Abu59673	Abo24863	Abu66868	Ada45565	Ada75996	Ada18646			Adb27595	Ada86074	Adb15638	Ada47424	Ada67219	Adb30226	Ada85522	Ada96734	Ada79038	Ada87177	Adb16379
TD CI	ADD95076	AAU12194	ABB77445	ABO17638	ABU80892	ABU66592	ABU59673	AB024863	ABU66868	ADA45565	ADA75996	ADA18646	ADA61269	ADB19054	ADB27595	ADA86074	ADB15638	ADA47424	ADA67219	ADB30226	ADA85522	ADA96734	ADA79038	ADA87177	ADB16379
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ADA91471	ADB14534	ADB18495	ADA93710	ADB19606	ADB12918	AB043171	ADA74172	ADB24405	ADA81929	ADA74892	ADA84970	ADA84418	ADB29674	ADA80202	ADA75444	ADA46669	ADB24965	ADA93141	ADB26491
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56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

480

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Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte; A-peptide; factor VIIA; gene therapy.
                                481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ
                                                                               TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ
               KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLOKYLKSKESVSHAILQTDQAL
                                                                                                                                             QXMQEQQMQVFINCFISPLPVTMRVCSSGKEGEAARSCGSQQGVMSQKVWV 591
                                                                                                                                                                                                                                                                                                                                                                Human PRO4987 polypeptide sequence.
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99WO-US030095.
99WO-US030911.
99WO-US030999.
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11-FEB-2000;
18-FEB-2000;
22-FEB-2000;
24-FEB-2000;
24-FEB-2000;
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20-DEC-1999;
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21-MAR-2000;
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17-MAY-2000;
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02-DEC-1999
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                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to the isolation of a novel human guanylate binding protein (guanylate binding protein-4 or GBP-4), and the binding protein by the sequence encoding it. The polymucleotide sequence encoding GBP-4, the GBP-4 polypeptide, and antibodies to GBP-4 are useful in treating myelodysplastic disorders, myeloproliferative syndromes, acute myeloid leukaemia and cancers (e.g. gastric, lung or colon cancers or malanoma). The polymucleotide sequence is useful as hybridisation probes, in chromosome and gene mapping, in generating transgenic animals, in radioimmunoassays, in inducing formation of anti-GBP-4 antibodies, in combating immunological and inflammatory responses and other pathological
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    conditions (e.g. multiple sclerosis or iung and intestinal-related disorders), as a mediator of any interferon-gamma-induced responses in macrophages and fibroblasts, and may also function in other immune cell populations or in protein processing. The present sequence represents
                                                                                                                                                                                                                                                                            New isolated nucleic encoding guanylate binding protein-4, useful as hybridization probes, in chromosome and gene mapping, treating cancer, e.g. gastric cancer or melanoma or combating immunological and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MALBIHMSDPMCLIENFNEQLKVNQEALBILSAITQPVVVVAIVGLYRTGKSYLMNKLAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV
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/note= "Specifically claimed in Claim 26"
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100.0%; Pred. No. 2.1e-241;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 3; 60pp; English
                                                                                                  17-AUG-2000; 2000US-00643657
                                                                                                                                 98US-00015089
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                                                                                                                                                                                                                                                                                                                   e.g. gastric cancer or
inflammatory responses.
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Best Local Similarity
Matches 591; Conserv
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                                                                                                                                 29-JAN-1998;
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

July 9, 2005, 13:18:54; Search time 172 Seconds (without alignments) 1759.528 Million cell updates/sec

Title: Perfect score: Sequence:

US-10-659-549-3 3043 1 MALEIHMSDPMCLIENFNEQ.....GEAARSCGSQQGVWSQKVWV 591

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 seqs, 512079187 residues Searched:

16,12378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

UniProt\_03:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\* Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	Q96pp8 homo sapien	homo	Q8nf03 homo sapien	homo	P32455 homo sapien	Q8bmn7 mus musculu	Q8cfb4 mus musculu	Q8bu78 mus musculu	P32456 homo sapien	homo	homo	Q01514 mus musculu	Q8tce5 homo sapien	Q63663 rattus norv	Q9z0e6 mus musculu	Q8n8v2 homo sapien	рошо	homo	homo	Q7z3f0 homo sapien	Q8bu48 mus musculu	Q6kan1 mus musculu	Q91z40 mus musculu	Q8vec5 mus musculu	Q61107 mus musculu	Q8cfa8 mus musculu	Q6zq18 mus musculu	Q9nv33 homo sapien	gn <sub>m</sub>	MUB	Q6pg83 mus musculu
	QI	GBP5 HUMAN	Q86TMS	Q8NF03	Q8N4Q4	GBP1 HUMAN	Q8BMN7	GBP5 MOUSE	Q8BU78	GBP2 HUMAN	Q6GP <u>H</u> 0	Q9H0R5	GBP1_MOUSE	QBTCES	GBP2 RAT	GBP2_MOUSE	Q8N8 <u>V</u> 2	99NZ9Ö	GBP4_HUMAN	Oens <u>r</u> o	Q7Z3F0	Q8BU48	Q6KAN1	Q91Z40	Q8VECS	Q61107	Q8CFA8	Q6ZQL8	Q9NV33	Q6PEN2	Q61594	Q6PG83
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ا مد	Match	92.5	82.7	81.8	73.5	64.4	63.5	62.7	62.6	62.3	62.2	58.3	58.0	58.0	57.8	57.5	50.2	49.6	49.3	49.2	49.1	48.7	48.7	48.6	48.3	48.0	46.2	45.8	45.6	45.3	44.9	44.2
	Score	2815	2516	2490	2236	1958.5	1933	1907.5	1905.5	1897	1892	1774.5	1765.5	1764	1757.5	1750.5	1528.5	1510.5	1500.5	1498.5	1493.5	1482.5	1482.5	1479.5	1468.5	1459.5	1407	1392.5	1388.5	1377.5	1365.5	1344
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^ = '	Q6dcg/ xenopus lae Q7t0s6 xenopus lae Q66j21 xenopus lae		Q8k0g1 mus musculu Q6p3v3 homo sapien Q90892 gallus gall	Q6pci2 xenopus lae Q7tmv8 mus musculu Q66k09 mus musculu
Q6GN80 Q8BTS3	Q6DCG7 Q7T0S6 Q66J21	Q66IR9 Q6YLY1 Q6DHP7	Q8K0G1 Q6P3V3 Q90892	Q6PC12 Q7TMV8 Q66K09
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332	4.0.0.0 4.0.0.0	39 39 39	4 4 4 0 1 2	4 4 4 6 4 6

## ALIGNMENTS

RESULT 1 GBPS HUMAN ID GBPS HUMAN STANDARD; PRT; 586 AA. AC 096PP8;		24422-04:10	RA 121 RA SEQUENCE FROM N.A., RA Eichmueller S., Hartmann T., Thiel D., Usener D., Dummer R., RA Schadendorf D.; R. Schadendorf D.; RT "GBP-TA: a new tumoy specific antigen of cutaneous lymphoma depicted RT by serological detection."; RY Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. RN 121	-02000000000000000000000000000000000000	- 01-204411
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                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millahy S.J., Bosak S.A., McKernan K.J., McKernan K.J., Malek J.A., Gunarathe P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Hulyk S.W., Villalon D.K., Muzny D.M., Sdergren B.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Schmetz A.C., Grimwood J., Schmutz J., Myers R.W., Schnerch A., Schein J.B., Jones S.J.M., Marra M.A., Schein J.B., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRIGKSYLANKLAG
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Pfam; PF02263; GBP; 1.
Pfam; PF02841; GBP; 1.
GTP-binding; Lipoprotein; Multigene family; Prenylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S-geranylgeranyl cysteine similarity). 95DDC02F0FB705D0 CRC64;
                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- SIMILARITY: Belongs to the GBP family.
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GTP (By similarity)
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Matches 549; Conservative
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EMBL; BC031639; AAH31639
HSSP; P32455; 1DG3.
Genew; HGNC:19895; GBP5.
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421 KOGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL
                             TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MALEIHMSDPMCLIENFNEQLKVNQBALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=14996095;
Hartmann T.B., Thiel D., Dummer R., Schadendorf D., Bichmuller S.;
"SEREX identification of new tumour-associated antigens in cutaneous
T.cell lymphoma.";
Br. J. Dermatol. 150:252-258(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fellenberg F., Hartmann T.B., Dummer R., Usener D., Schadendorf D., Eichmuller S.; "GBP-5 splicing variants: New guanylate-binding proteins with tumor-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82.7%; Score 2516; DB 2; 99.8%; Pred. No. 1.8e-119; rative 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     associated expression and antigenicity.";
J. Invest. Dermatol. 122:1510-1517(2004).
EMBL; AF138777; AA040731.1;
HSSP, P34455; 1DG3.
GO; GO:0005525; F:GTP binding; IEA.
GO; GO:000524; F:GTPase activity; IEA.
GO; GO:000595; P:immune response; IEA.
InterPro; IPR003191; GBP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTCL tumor antigen GBP-5ta (Fragment).
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TISSUE=Cutaneous lymphoma;
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Pfam, PF02841; GBP_C; 1.
NON TER 489 489
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                                                                                                                                                                                                     541 QKMQEQQMQ 549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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SEQUENCE
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us-10-659-549-3.rup

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KDIFGPLEBAVKQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESV 469
                                                                                       EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420
                                                                                                       BAIEVFWKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 441
                                                                                                                                                   KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480
                                                                                                                                                                    442 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RLKNLVLTYVNAISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQOMGQKVQLPMETLQ 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELLDLHRISEREAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALL 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELLDLHRTSEREAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALL 304
HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 321
                                                  KKKCFIFDLPAHQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGS
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-DAR-2004 (TrEMBLrel. 26, Last annotation update)
Similar to quantylate binding protein 5 (Fragment).
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 2236; DB 2;
Pred. No. 2.6e-105;
1; Mismatches 0;
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Submitted (JUL-2002) to the EMBL/GenBank/Submitted (JUL-2002) to the EMBL/GenBank/HSSP; P32455; 1DG3.
GO: GO:0005525; F:GTP binding; IEA.
GO; GO:0005924; F:GTPsee activity; IEA.
GO; GO:0005924; F:GTPsee activity; IEA.
InterPro; IPR093191; GBP.
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99.8%;
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Best Local Similarity 99.89
Matches 439; Conservative
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Pfam; PF02841; GBP_C; 1.
NON TER 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300
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HQKKLAQLETLPDDELEPBFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN
               241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN
                                                                            AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER
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                                                                                                                     EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV
                                                                                                                                     KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL
                                                             AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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TISSUE-Spleen,
Jikuya H., Takano J., Kikuno R., Nagase T., Ohara O.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AK090491; BAC03460.1; -.
HSSP; P32455; 1DG3.
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01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2004 (TrEMBLrel. 26, Last annocation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81.8%; Score 2490; DB 2; L
100.0%; Pred. No. 3.9e-118;
ive 0; Mismatches 0;
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GO; GO:0003924; F:GTPase activity; IEA.
GO; GO:0006955; P:immune response; IEA.
InterPro; IPR003191; GBP.
Pfam; PF02263; GBP; 1.
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Best Local Similarity 100.º
Matches 483; Conservative
                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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TETEKKKKK 489
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SEQUENCE
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Richards R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A paperon M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Frange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Brownstein M.J., Widnin T.B., Tooshiyuki S., Carninci P., Prange C.,
A Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Brichards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smallus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smallus D.E.,
Browner C. A., Generation and initial analysis of more than 15,000 full-length human
                        SHAILQTDQALTETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMNQERERLHQEQVRQM 529
305 KDIFGPLEEAVKQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESV 364
                                                                                                                                                                                               01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
25-0CT-2004 (Rel. 45, Last annotation update)
Interferon-induced guanylate-binding protein 1 (GTP-binding protein 1) (Guanine nucleotide-binding protein 1) (HuGBP-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nantais D.E., Schwemmle M., Stickney J.T., Vestal D.J., Buss J.E.;
"Prenylation of an interferon-gamma-induced GTP-binding protein: the human guanylate binding protein, huGBPl.";
J. Leukoc. Biol. 60:423-431(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S., Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                           MEDLINE=91342675; PubMed=1715024;
Cheng Y.-S.E., Patterson C.E., Staeheli P.;
"Interferon-induced quanylate-binding proteins lack an N(T)KXD
consensus motif and SMP in addition to GDP and GTP.";
Mol. Cell. Biol. 11:4717-4725(1991).
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MEDLINE-22388257; PubMed-12477932; DOI-10.1073/pnas.242603899;
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                                                                                           WEDLINE=96427476; PubMed=8830800;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                         Prakash B., Praefcke G.J.K., Renault L., Wittinghofer A., Herrmann C. "Structure of human guanylate-binding protein 1 representing a unique
                                                                                 class of GTP-binding proteins.";
Nature 403:567-571(2000).
--- FUNCTION: Binds GTP, GDP and GMP.
--- INDUCTION: By interferon gamma during macrophage activation.
--- SIMILARITY: Belongs to the GBP family.
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EMBL; BC002666; AAH02666.1; -.
PIR; A41268; A41268.
PDB; IDG3; X-ray; A=1-592.
PDB; IFSN; X-ray; A=1-592.
Genew; HGNC:4182; GBP1.
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t male pituitary gland cDNA, RIKEN full-length clone:5330409506 product:weakly similar to GUANYLATE
full-length
                                                                                                EDNA cloning.";
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GO; GO:0005525; P:GTP binding; IEA.
GO; GO:0003924; P:GTPase activity; IEA.
                                                                                        Carninci P., Hayashizaki Y., "High-efficiency full-length (Meth. Enzymol. 303:19-44(1999)
musculus adult
       enriched library, a BINDING PROTEIN 5.
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Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W., Hukuda S., Furuno M., Haragaki T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., Hayashida K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Kolone H., Konno H., Konno H., Kouda M., Koya S., Kurihara C., Marsuka T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saitoh H., Saatal C., Sakai K., Sakai M., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Towaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y., Lomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y., Rubbi tted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

HSSP: P32455; 1DG3. SEQUENCE FROM N.A.
STRANIE-STREL/GAJ TISSUE-Pituitary gland;
The FANTOM Consortium.
The RIKEN Genome Exploration Research Group Phase I & II Team;
Thanalysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAB,";
Nature 420:563-573(2002). SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Pituitary gland;
STRAIN=C57BL/6J; TISSUE=Pituitary gland;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Mornalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraties for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2006). . STRAIN=C57BL/6J; TISSUE=Pituitary gland; MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; STRAIN-C57BL/63; TISSUE-Pituitary gland;
MEDLINE-20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matumioto H., Sakaguchi S., Ikegami T., Kabliwagi K.,
Fujiwake S., Inoue K., Togawa W., Izawa M., Ohara E., Watshiwagi K.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RIKIS integrated sequence analysis (RISA) system-384-format
Genome Res. 10:1757-1771(2000) Mus musculus (Wouse). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus NCBI\_TaxID=10090; "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2002). SEQUENCE FROM N.A. STRAIN-GSPBL/60; TISSUE=Pituitary gland; MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500; RIKEN FANTOM COMSORTIUM;

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QBCFB4; QBCFA4;
29-MAR-2004 (Rel. 43, Created)
29-MAR-2004 (Rel. 44, Last sequence update)
05-MOL-2004 (Rel. 44, Last annotation update)
Interferon-induced guanjlate-binding protein 5 (GTP-binding protein (Guanine nucleotide-binding protein 5) (MuGBP-5).
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STRAIN=Swiss Webster;
MEDLINE=22284156; PubMed=12396730; DOI=10.1089/107999002760274926;
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                              Length 724;
                                                                                                            63.5%; Score 1933; DB 2; Length 7 64.9%; Pred. No. 8.8e-90; ive 70; Mismatches 126; Indels
                                                                         799C517B51DBF47C CRC64;
GO; GO:0006955; P:immune response; IEA.
InterPro; IPR003191; GBP.
Pfam; PF02263; GBP; 1.
Pfam; PF02841; GBP C; 1.
SEQUENCE 724 AA; 80410 MW; 799C517E
                                                                                                                               Best Local Similarity 64.9
Matches 392; Conservative
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ACADEMONE, ALCADESTREASE CUMOST,
ALCADESTREASE, 1120-12477932; DOI=10.1073/pnas.242603899;
ALCADESTREASE, PubMed=12477932; DOI=10.1073/pnas.242603899;
ALCADER R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B. Buetcow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B. Buetcow K.H., Schaefer C.F., Bhat N.K.,
A mischenko, Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M.J., Usdin T.B., Donaldo M.F., Casavant T.L., Scheetz T.E.,
A Rapleton M., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,
A Rapleton M., Worley N., Peters G.J., Abramson R.D., Mullahy S.J.,
Brownstein M.J., WcKernan K.J., Malek J.A., Gunaratne P.H.,
A Bask S.S., McKwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,
A Pahey J., Helton B., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S. N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S. N., Krzywinski M.I., Skalska U., Smailus D.E.,
Browner A., Schein J.E., Jones S.J.M., Marra M.A., Solentarion and initial analysis of more than 15,000/full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Nguyen T.T., Hu Y., Widney D.P., Mar R.C., Smith J.B.; "Murine GBP-5, a new member of the murine guanylate-binding protein family, is coordinately regulated with other GBPs in vivo and in vitro.";
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Pred. No. 1.3e-88;
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GTP (By similarity).
S-geranylgeranyl cysteine (By similarity).
KX -> T (in Ref. 2).
K -> E (In Ref. 2).
W, 092C0B3F3E0E2D26 CRC64;
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Interpro; IPR003191; GBP.
Pfam; PF02263; GBP; 1.
Pfam; PF02841; GBP_C; 1.
GTP-binding; Lipoprotein; Multigene family; Prenylation.
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SEQUENCE FROM N.A.
Adams M., Mural R.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
-!- SIMILARITY: Belongs to the GBP family.
                                                                                                                                                                        Interferon Cytokine Res. 22:899-909 (2022)
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=NMRI; TISSUE=Breast tumor;
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EMBL, FAY128412; AAN46362.1; -.
EMBL, BCO58555; AAH58555.1; -.
HSSP; P32455; IDG3.
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240 PALGSKLSQLPTLSNEELNSDFVQDLSEFCSHIFTQSKTKTLPGGIQVNGPRLESLVLTY
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                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 0 day neonate lung cDNA, RIKEN full-length enriched
library, clone:E030025M22 product:weakly similar to GUANYLATE BINDING
PROTEIN 5 (Fragment)
                                TLRDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDL
                                                                        PAHOKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTY
                                                                                                               VNAISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTS
                                                                                                                                                       EREAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEE
                                                                                                                                                                                               AVKQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=C57BL/6J; TISSUE=Lung;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length DNA cloning.";
Meth. Enzymol. 303:19-44(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the RIKEN Genome Exploration Research Group Phase I & II Team; Analysis of the mouse tyanscriptome based on functional annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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STRAIN=C57BL/6J; TISSUE=Lung;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRALM-C57BL/6J; TISSUE=Lung;
MEDLINE=21.085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM COMBORTLUM;
                                                                                                                                                                                                                                                                                                                                                       561 AA
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STRAIN-G57BL/6J; TISSUE-Lung;
The FANTOM CONSOCTIUM,
the RIKEN GENOME Exploration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60,770 full-length cDNAs/";
Nature 420:563-573(2003/).
                                                                                                                                                                                                                                                                               534 - ONWLAEQOKMOE 545
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EQQWILKQRAQEE 552
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01-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=C57BL/6J; TISSUB=Lung;
Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,
Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,
A Fukuda S., Furnoo M., Hanagaki T., Hara A., Hashizume T.,
A Hayashida K., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
A Hori F., Imotani Y., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
Nishi K., Nomura K., Mumazaki R., Ohno M., Ohato N., Okazaki Y.,
A Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.

REMBL, AKO87083; BAS39801.1; -.
Carninci P., Shibata Y., Hayateu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramateu M., Hayashizaki Y.; Wormalization and subtraction of Cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630 (2000)
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                                                                                                                                                                                                                              SECURALE FOR MAINTIESURE-LUNG;
MEDLINE-20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Ttoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Ttoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Yoneda Y., Ishikawa T., Cawa K., Izawa M., Ohara E., Watahiki M., Yoneda Y., Inhikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Ozawa Y., Harada M., Hayashizaki Y.; Rizaki Y., Murameteu M., Ilone Y., Kira A., Hayashizaki Y.; Bequencing pipeline with 384 múlticapillary sequencer.";
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69.0%; Pred. No. 1.6e-88;
ive 60; Mismatches 108; Indels
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GO; GO:0005525; F:GTP binding; IEA.
GO; GO:0005525; F:GTPase activity; IEA.
GO; GO:0006955; P:immune response; IEA.
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Matches 380; Conservative
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Pfam; PF02263; GBP; 1.
Pfam; PF02841; GBP_C; 1.
NON_TER 561 561
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241 PKKYLAHLEQLKEEELNPDFIEQVAEFCSYILSHSNVKTLSGGIAVNGPRLESLVLTYVN 300
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                   induction; Lipoprotein; Multigene family;
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-----RLLKEGFENESKR----LQKDIW
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TISSUESKin;
MEDILINE=22388257; PubWed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
                                                                                                                                                                                                                                         88; Mismatches 101; Indels
                                                         GTP (By similarity).
GTP (By similarity).
S-geranylgeranyl cysteine similarity).
                                                                                                                                        S -> G (in Ref. 3).
E090809EE18FC8A8 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Guanylate binding protein 2, interferon-inducible.
Name-GBP2;
                                                                                                                                                                                                   Score 1897; DB 1;
Pred. No. 4.6e-88;
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ilarity 63.5%;
Conservative 88
            GTP-binding, Interferon in Prenylation. 45 52 NP BIND 97 101 LIFID 588 588
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Pfam; PF02841; GBP
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Best Local Simi
Matches 377;
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                                                                                                                                        CONFLICT
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                                                                                                                                                                                    ALTETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLA 538
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                       EREAI EVFMKNS FKDVDQS FQKELETLLDAKQND I CKRNLEASSDYCSALLKD I FGPLEE
                                                                                                   AVKQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQ
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P32456; Q8GTB0;
01-0CT-1993 (Rel. 27, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Interferon-induced guanylate-binding protein 2 (GTP-binding protein 3 (Guanine nucleotide-binding protein 2)
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Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
Mewes H.-W., Weil B., Amid C., Fobo G., Han M., Osanger A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Binds GTP, GDP and GMP.
-!- INDUCTION: By interferon gamma during macrophage activation.
-!- SIMILARITY: Belongs to the GBP family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=91342675; PubMed=1715024; Cheng Y.-S.B., Patterson C.E., Staeheli P.; Cheng Y.-S.B., Patterson C.E., Staeheli P.; Interferon-induced guanylate-binding proteins lack an N(T)KXD consensus motif and bind GMP in addition to GDP and GTP."; Mol. Cell. Biol. 11:4717-4725(1991).
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EMBL; AL832451; CAD89925.1; -
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EQQWILKQRAQ 550
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HSSP; P32455; 1DG3.
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Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hslah F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch J.E.,
Jones S.J., Marra M.A.;
T. "Generation and initial analysis of more than 19,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC073163; AAH73163.1; -.
GO; GO:000525; F:GTP binding; IEA.
GO; GO:0003924; F:GTPase activity; IEA.
GO; GO:0006955; P:immune response; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003191; GBP.
Pfam; PF02263; GBP; 1.
Pfam; PF02841; GBP C; 1.
SEQUENCE 591 AA; 67233 MW; 739CE562AF335776 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                       and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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LAEQQ-----KMQEQQMQVFINCFISPLPVTMRVCSSGKEGEAARSCGSQQGVW 585
                                       ----RLLKEGFENESKR---LOKDIW 575
                                                                                                                                                                                                                                                                                                                                                                                                                                 The German cDNA Consortium;
Ottenwalder B., Obermaler B., Deutschenbaur S., Schaipp A.,
Ottenwalder B., Obermaler B., Deutschenbaur S., Schaipp A.,
Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann Submitted (ESP-1004) to the EMBL/GenBank/DDBJ databases.
EMBL, AL136680; CAB66615.1; -.
HSSP; P32455; 1DG3.
Genew; HGNC:4184; GBP3.
GO; GO:0005525; F:GTP binding; IEA.
GO; GO:0005525; P:GTP binding; IEA.
GO; GO:0005555; P:immune response; IEA.
                                                                                                                                                                                                                                                                                                                 Craniata, Vertebrata, Euteleostomi,
Catarrhini, Hominidae, Homo.
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OF 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
OI-MAR-2004 (TrEMBLrel. 26, Last sequence update)
E Hypothetical protein DKFZp564C2478.
Name=DKFZp564C2478;
S Homo sapiens (Human)
E Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; But Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Ho. 171 (1)
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Pfam; PF02263; GBP; 1.
Pfam; PF02841; GBP_C; 1.
SEQUENCE 563 AA; 64127 MW; OCZFB7CE7FFCBCC3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58.3%; Score 1774.5; DB 2; 65.4%; Pred. No. 6.8e-82; ive 61; Mismatches 90;
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                        Best Local Similarity 65.49
Matches 363; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Brain;
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TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQ----MEIAKQNW 536
                         01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Interferon induced guanylate-binding protein 1 (GTP-binding protein 1)
Guannine nucleotide-binding protein 1) (mGBP1) (mGBP-1) (Interferongamma inducible protein MAG-1).
Name=Gbp1; Synonyms=Gbp-1, Mag-1, Mpa1;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stickney J.T., Buss J.E.; "Murine guanylgeranyl isoprenoid modification of an interferon-gamma-inducible guanosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=92091752; PubMed=1753106; Wynn T.A., Nicolet C.M., Paulnock D.M.; Tidentification and characterization of a new gene family induced during macrophage activation."; J. Immunol. 147:4384-4392(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        triphosphate-binding protein.;

Mol. Biol. Cell 11:2191-2200(20dp).

-! FUNCTION: Binds GTP, GpP and Guring macrophage activation.

-! FUNCTION: By interferon gamma during macrophage activation.

-!- PTM: Prenylation of mouse GBP1 is incomplete. It persistently exists in the cell as a mixture of C20-modified and (more predominantly) nonmodified form.

-!- SIMILARITY: Belongs to the GBP family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=91342675; PubMed=1715024;
Cheng Y.-S.E., Patterson C.E., Staeheli P.;
Interferon-induced guanylate-binding proteins lack an N(T)
consensus motif and bind GMP in addition to GDP and GTP.";
Mol. Cell. Biol. 11:4717-4725(1991).
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InterPro; IPR003191; GBP.
Pfam; PF02263; GBP; 1.
Pfam; PF02841; GBP_C; 1.
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HSSP; P32455; 1DG3.
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GBP1 MOUSE
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SEQUENCE FROM N.A.
TISSUE=Lung;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsich F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Staplecton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
                                                                                                                                                                                                                                                         Gaps
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
S-geranylgeranyl cysteine (partial)
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95; Mismatches 109;
                                                                                                                                                 58.0%; Score 1765.5; D 61.7%; Pred. No. 2e-81;
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541 MAEQQRIISLKLQEQE 556
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Homo sapiens (Human)
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Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield X.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;
                                                                                                                                                                                                                                                                                                                                   KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL
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                                                                                                                                              Strausberg R.;
Strausberg R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC022272; AAH22272.1; --
HSSP; P32455; 1DG3.
GO; GO:0005525; F:GTP binding; IEA.
GO; GO:0003924; F:GTPase activity; IEA.
GO; GO:0006955; P:immune response; IEA.
                                                                                                                                                                                                                                                           54034 MW; 2F8B66BEA92EED87 CRC64;
                                                                                              and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Pfam; PF02263; GBP; 1.
Pfam; PF02841; GBP_C; 1.
SEQUENCE 481 AA; 54034
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(Rel. 43, Created) (Rel. 43, Last sequence update)

063663; 29-MAR-2004 29-MAR-2004

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                                                                                                                                             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalla, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
DS-JUL-2004 (Rel. 44, Last annotation update)
Interferon-induced guanylate-binding protein 2 (GTP-binding protein (Guannine nucleotide-binding protein 2) (p67).
                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND ISOPRENOID.
MEDIATE-941981297; PubMed=8148170; DOI=10.1016/0167-4781(94)90284-4;
ASSUNDIA V.S., STahl R.C., Showalter L., Conner K.J., Carey D.J.;
"Molecular cloning and characterization of an isoprenylated 67 kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, M80367; AAA19909.1; ALT_INIT.
PIR; S43506; S43506.
HSSP; P32455; 1DG3.
HTGFPFO: PF002263; GBP.
Pfam; PF002263; GBP; 1.
Pfam; PF022841; GBP_C; 1.
Pfam; PF02841; GBP_C; 1.
GTP-binding; Interferon induction; Lipoprotein; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 589;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57.8%; Score 1757.5; DB 1; Length
63.3%; Pred. No. 5.2e-81;
tive 82; Mismatches 116; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52 GTP (By similarity).
101 GTP (By similarity).
586 S-geranylgeranyl cysteine.
67109 MW, 5E52B79102C2D97F CRC64;
                                                                                                                                                                                                                                                                                                                                                             protein.";
Biochim. Biophys. Acta 1217:257-265(1994).
-!- FUNCTION: Binds GTP, GDP and GMP (By similarity).
-!- TISSUE SPECIFICITY: Ubiquitous.
-!- INDUCTION: By interferon gamma.
-!- SIMILARITY: Belongs to the GBP family.
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Matches 346; Conservative
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101
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                                                                                                                       Rattus norvegicus
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NP_BIND
LIPID
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Ratausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Ratausperg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Uddin T.B., Toshlyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S.W. Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahay J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 480
                                                                                      537
                6
KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL
                                                         TETEKKKKEAQVKAEAEKAEAQRLAA1QRQNEQMMQERERLHQEQVRQME1AKQNWLAEQ
                                                                        늉
                                                                                                                                                                                                                                                                                   (GTP-binding protein (mGBP-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND ISOPRENOID.
STRAIN=C57BL/6; TISSUE=Bone marrow;
MEDLINE=99074031; PubMed=9858320;
Vestal D.J., Buss J.E., McKercher S.R., Jenkins N.A., Copeland N.G.
Kelner G.S., Asundi V.K., Maki R.A.;
"Murine GBP-2: a new IFN-gamma-induced member of the GBP family of GTPases isolated from macrophages."
                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=CS7BL/6;
MEDLINE=99077537; PubMed=9862701;
Doben U., Guethlein L., Klamp T., Ozbek K., Schaub A., Fuetterer A.
Pfeffer K., Howard J.C.,
"Two families of GTPases dominate the complex cellular response to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anderson S.L., Carton J.M., Zhang X., Rubin B.Y.; Garton or corganization and chromosomal localization of a new member the murine interferon-induced guanylate-binding protein family."; J. Interferon Cytokine Res. 19:487-494 (1999).
                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Kidney;
MEDLINE=99313432; PubMed=10386861; DOI=10.1089/107999099313938;
                                                                                                                                                                                                                  GBP2_MOUSE STANDARD; PRT; 589 AA.
Q9Z0E6; Q8CLC6; Q921N2; Q9R110;
29-MAR-2004 (Rel. 43, Created)
29-MAR-2004 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Interferon-induced guanylate-binding protein 2
(Guanine nucleotide-binding protein 2) (mGBP2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTPases isolated from macrophages.";
J. Interferon Cytokine Res. 18:977-985(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IFN-gamma.";
J. Immunol. 161:6715-6723(1998)
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Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MASEIHMSEPMCLIENTEAQLVINQEALRILSAITQPVVVVAIVGLYRTGKSYLMNKLAG
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NP BIND 45 52 GTP (By similarity).

NP_BIND 97 101 GTP (By similarity).
                                           and mouse CDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

-! FUNCTION: Buinds GTP, GDP and GMP (By similarity).

-! INDUCTION: By interferon gamma during macrophage activation.

-! SIMILARITY: Belongs to the GBP family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52 GTP (By similarity).
101 GTP (By similarity).
586 S-geranylgeranyl cysteine.
163 V -> I (in Ref. 4).
246 S -> T (in Ref. 3).
248 S -> T (in Ref. 3).
249 E -> D (in Ref. 3).
240 BE68BOA3BCSF3AE3 CRC64;
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84; Mismatches 114; Indels
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                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AJ007970; CAA07797.1; -. EMBL; AF077007; AAC98287.1; -. EMBL; AF109168; AAD3946.1; -. EMBL; BC011336; AAH11336.1; -. EMBL; BC032882; AAH32882.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P32455; 1DG3.
MGD; MGI:102772; Gbp2.
InterPro; IPR003191; GBP.
Pfam; PF02263; GBP; I.
Pfam; PF02841; GBP C; I.
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Matches 349; Conservative
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